



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:02 PM UTC

PDB ID : 9ZRG / pdb\_00009zrg  
EMDB ID : EMD-74615  
Title : Structure of naked mole-rat ribosome (non-rotated)  
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.  
Deposited on : 2025-12-19  
Resolution : 3.10 Å(reported)  
Based on initial model : 4V6X

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

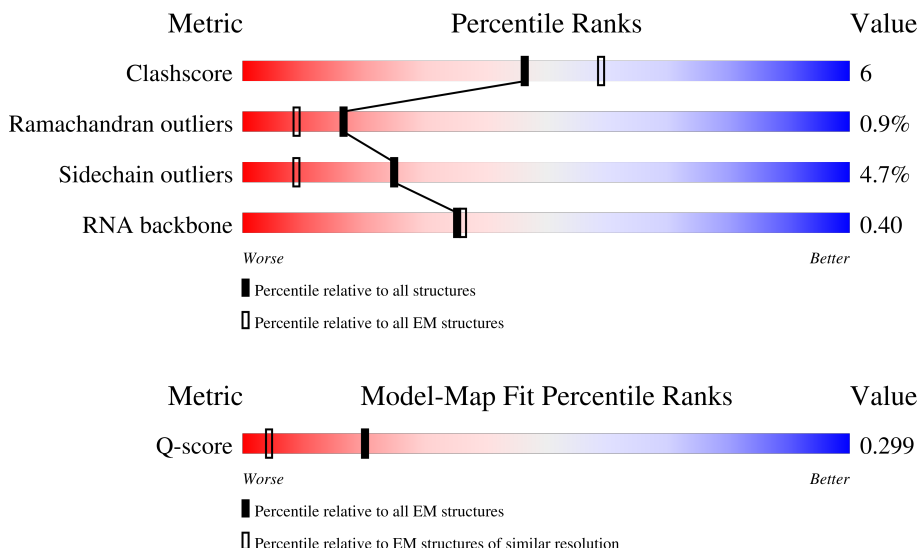
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.









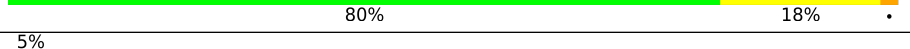
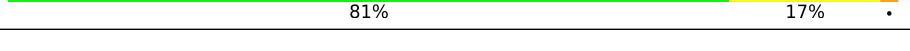
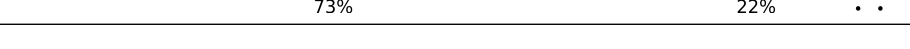
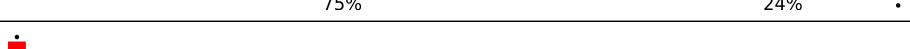
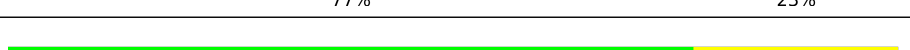

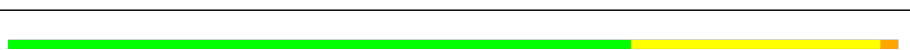

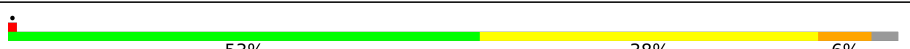





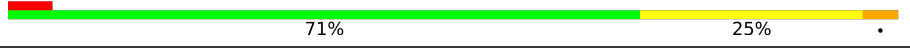
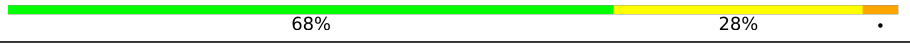



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 ( 2.60 - 3.60 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AO	136	
2	AX	142	
3	AN	150	










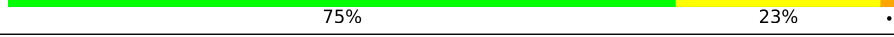

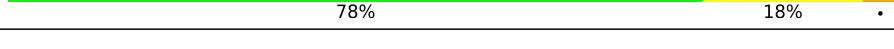
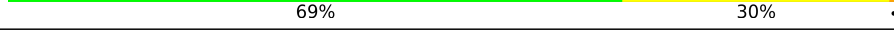
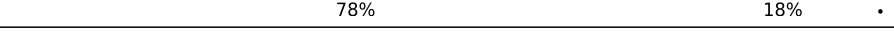
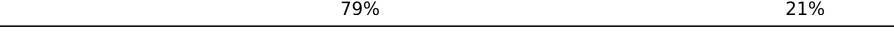


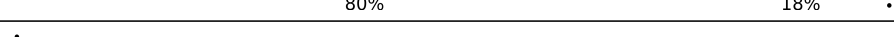




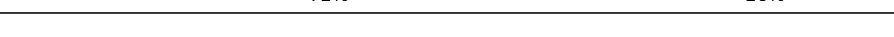
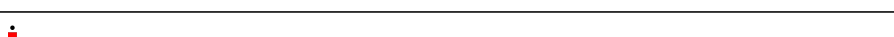

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Mol	Chain	Length	Quality of chain
4	AL	158	
5	AB	215	
6	AA	208	
7	AV	82	
8	AY	126	
9	Aa	107	
10	Ab	84	
11	Ae	59	
12	AJ	182	
13	AE	263	
14	AC	226	
15	AG	237	
16	AH	190	
17	AW	129	
18	AI	206	
19	B2	1861	
20	CR	153	
21	CW	124	
22	Ag	313	
23	AU	104	
24	AK	98	
25	AM	124	
26	AS	137	
27	Ad	53	
28	AR	126	







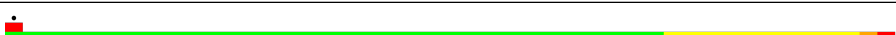
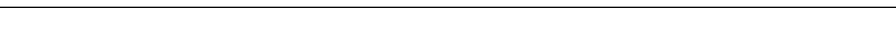
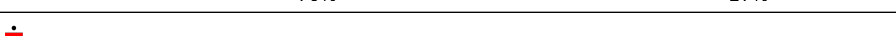
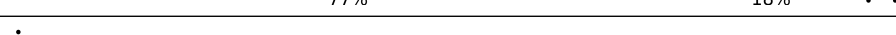
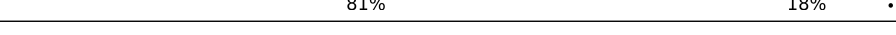
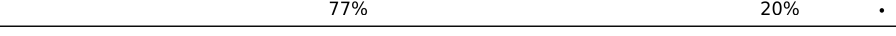













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Mol	Chain	Length	Quality of chain
29	AP	127	
30	AT	141	
31	AZ	75	
32	Ac	64	
33	AD	227	
34	Af	71	
35	AF	191	
36	AQ	141	
37	Cz	217	
38	CO	202	
39	CL	210	
40	CV	133	
41	CM	139	
42	Ca	147	
43	CN	203	
44	CI	213	
45	CD	289	
46	CQ	188	
47	CA	255	
48	CS	175	
49	CT	159	
50	CP	152	
51	CU	112	
52	CX	121	
53	CY	133	


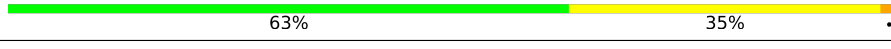
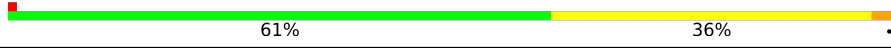

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Mol	Chain	Length	Quality of chain
54	CZ	135	
55	Cr	137	
56	Ch	123	
57	Cb	78	
58	CB	397	
59	CF	229	
60	Cc	100	
61	Cd	113	
62	Ce	133	
63	Cf	109	
64	Cg	114	
65	Ci	103	
66	Cj	90	
67	Ck	69	
68	Cl	50	
69	CC	368	
70	Cm	52	
71	Cn	25	
72	Cp	90	
73	Co	105	
74	CJ	168	
75	CH	191	
76	CE	262	
77	CG	246	
78	A5	3889	

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Mol	Chain	Length	Quality of chain
78	A6	3889	
79	A7	121	
80	A8	157	
81	BC	75	

## 2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 219292 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 2 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AX	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 3 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 4 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AL	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 5 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	215	Total	C	N	O	S	0	0
			1747	1110	313	310	14		

- Molecule 6 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 7 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 8 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 9 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 10 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ab	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 11 is a protein called Ubiquitin-like protein FUBI.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ae	59	Total	C	N	O	S	0	0
			468	290	102	75	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AJ	175	Total	C	N	O	S	0	0
			1463	933	292	236	2		

- Molecule 13 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AE	263	Total	C	N	O	S	0	0
			2084	1329	387	359	9		

- Molecule 14 is a protein called 40S ribosomal protein S2.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	AC	226	Total	C	N	O	S	0	0
			1751	1130	301	310	10		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 16 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AH	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 18 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 19 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	B2	1799	Total	C	N	O	P	0	0
			37803	16849	6724	12432	1798		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CR	153	Total	C	N	O	S	0	0
			1257	780	265	206	6		

- Molecule 21 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 22 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ag	306	Total	C	N	O	S	0	0
			2387	1506	417	452	12		

- Molecule 23 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AU	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 24 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AM	124	Total	C	N	O	S	0	0
			960	600	171	181	8		

- Molecule 26 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 27 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ad	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 28 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AR	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 29 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AP	119	Total	C	N	O	S	0	0
			992	631	187	167	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AT	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 32 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ac	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 33 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AD	223	Total	C	N	O	S	0	0
			1736	1107	312	310	7		

- Molecule 34 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Af	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 35 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 36 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 37 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Cz	192	Total	C	N	O	S	0	0
			1534	981	274	271	8		

- Molecule 38 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CO	202	Total	C	N	O	S	0	0
			1655	1066	322	262	5		

- Molecule 39 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 40 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CV	133	Total	C	N	O	S	0	0
			989	623	186	175	5		

- Molecule 41 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CM	139	Total	C	N	O	S	0	0
			1139	730	218	183	8		

- Molecule 42 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ca	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 43 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 44 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CI	201	Total	C	N	O	S	0	0
			1626	1032	313	268	13		

- Molecule 45 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CD	289	Total	C	N	O	S	0	0
			2353	1483	429	427	14		

- Molecule 46 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CQ	188	Total	C	N	O	S	0	0
			1521	949	315	251	6		

- Molecule 47 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CA	255	Total	C	N	O	S	0	0
			1957	1225	399	327	6		

- Molecule 48 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 49 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 50 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CP	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 51 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CU	112	Total	C	N	O	S	0	0
			921	583	159	177	2		

- Molecule 52 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CX	121	Total	C	N	O	S	0	0
			994	636	187	170	1		

- Molecule 53 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CY	133	Total	C	N	O	S	0	0
			1107	695	225	185	2		

- Molecule 54 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 55 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Cr	137	Total	C	N	O	S	0	0
			1104	682	231	185	6		

- Molecule 56 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ch	123	Total	C	N	O	S	0	0
			1023	646	206	169	2		

- Molecule 57 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Cb	67	Total	C	N	O	S	0	0
			554	341	121	89	3		

- Molecule 58 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CB	392	Total	C	N	O	S	0	0
			3161	2014	593	540	14		

- Molecule 59 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CF	229	Total	C	N	O	S	0	0
			1910	1226	370	305	9		

- Molecule 60 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cc	100	Total	C	N	O	S	0	0
			776	492	136	141	7		

- Molecule 61 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Cd	113	Total	C	N	O	S	0	0
			931	586	181	162	2		

- Molecule 62 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Ce	133	Total	C	N	O	S	0	0
			1096	691	224	175	6		

- Molecule 63 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Cf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 64 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Cg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 65 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ci	103	Total	C	N	O	S	0	0
			840	526	178	130	6		

- Molecule 66 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cj	90	Total	C	N	O	S	0	0
			733	451	162	115	5		

- Molecule 67 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ck	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 68 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cl	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 69 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	CC	358	Total	C	N	O	S	0	0
			2853	1797	570	473	13		

- Molecule 70 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.



Mol	Chain	Residues	Atoms					AltConf	Trace
70	Cm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 71 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Cn	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 72 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Cp	90	Total	C	N	O	S	0	0
			703	442	135	119	7		

- Molecule 73 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Co	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 74 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CJ	168	Total	C	N	O	S	0	0
			1349	853	251	239	6		

- Molecule 75 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	CH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 76 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CE	262	Total	C	N	O	S	0	0
			2113	1357	403	349	4		

- Molecule 77 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	CG	246	Total	C	N	O	S	0	0
			1973	1256	379	334	4		

- Molecule 78 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A5	1720	Total	C	N	O	P	0	0
			36244	16105	6607	11813	1719		
78	A6	2169	Total	C	N	O	P	0	0
			44180	19585	7784	14642	2169		

- Molecule 79 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	A7	121	Total	C	N	O	P	0	0
			2578	1150	458	850	120		

- Molecule 80 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	A8	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

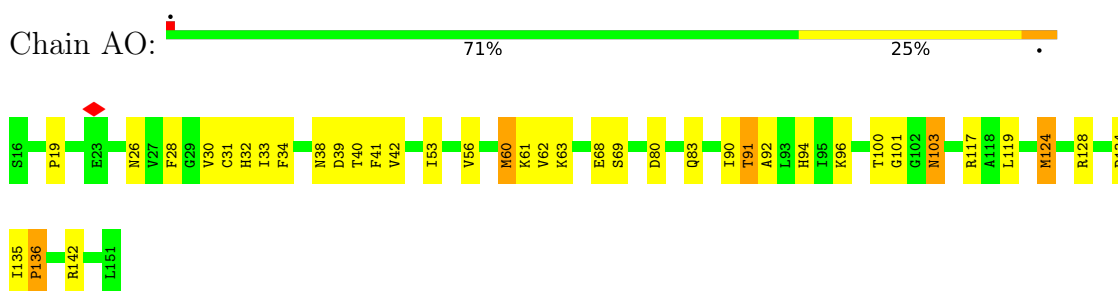
- Molecule 81 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BC	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

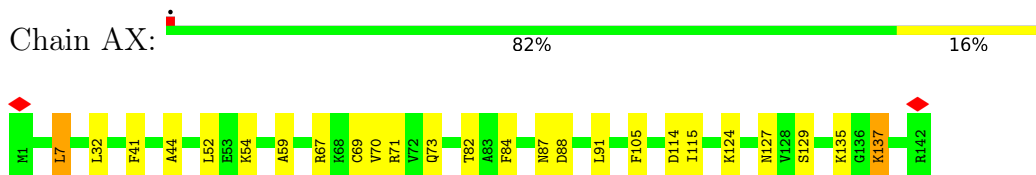
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

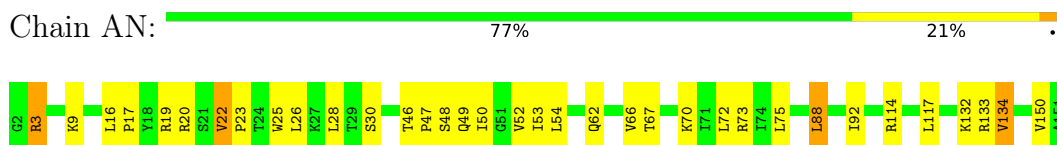
- Molecule 1: 40S ribosomal protein S14



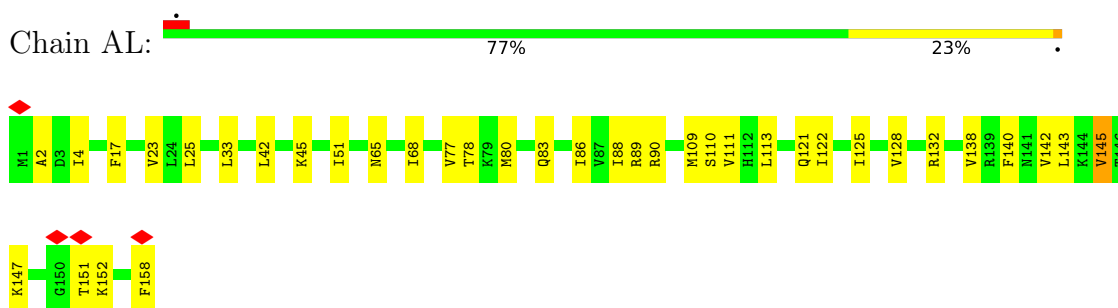
- Molecule 2: Small ribosomal subunit protein uS12




- Molecule 3: Small ribosomal subunit protein uS15

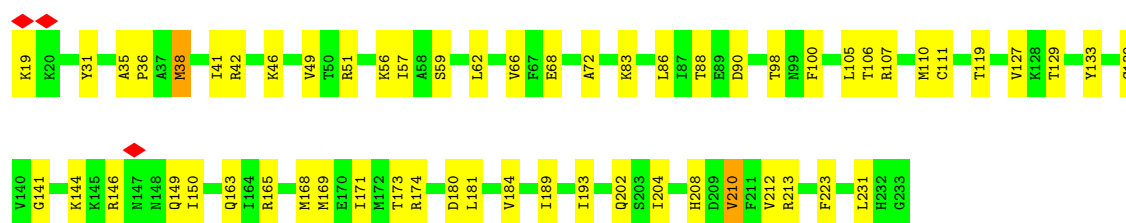


- Molecule 4: Small ribosomal subunit protein uS17




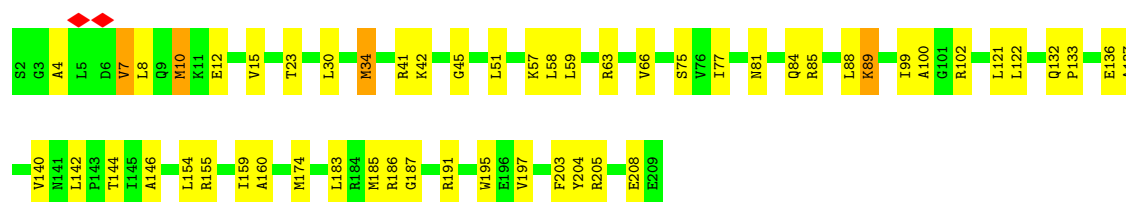
- Molecule 5: Small ribosomal subunit protein eS1

Chain AB:  73% 26%



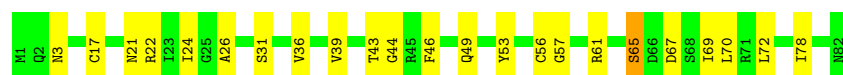
- Molecule 6: Small ribosomal subunit protein uS2

Chain AA:  74% 24%



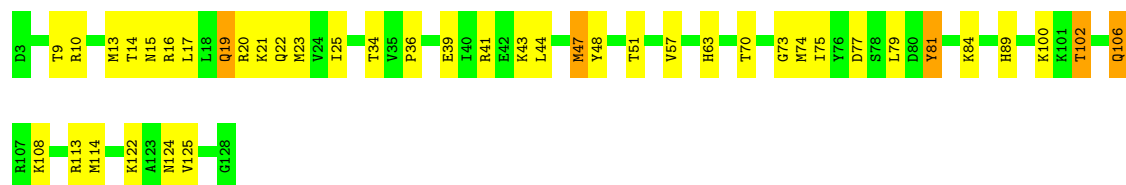
- Molecule 7: 40S ribosomal protein S21

Chain AV:  72% 27%




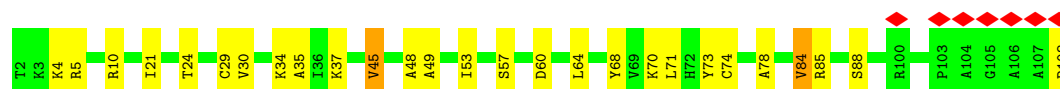
- Molecule 8: 40S ribosomal protein S24

Chain AY:  67% 29%




- Molecule 9: 40S ribosomal protein S26

Chain Aa:  7% 75% 23%

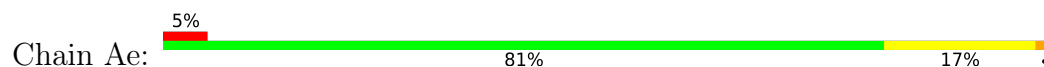


- Molecule 10: 40S ribosomal protein S27

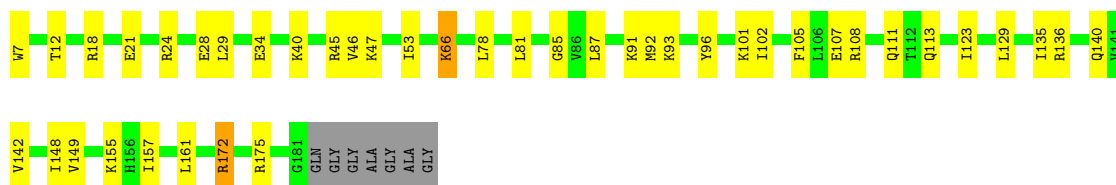
Chain Ab:  80% 18%



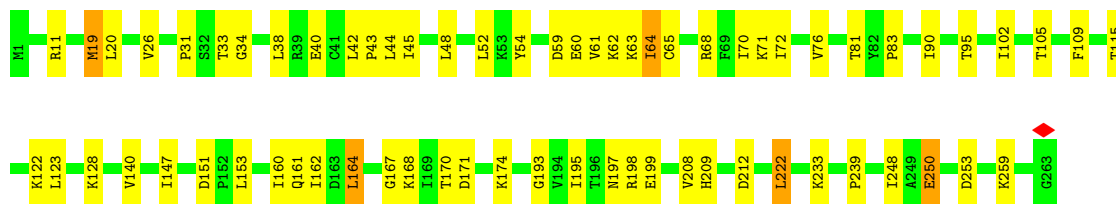
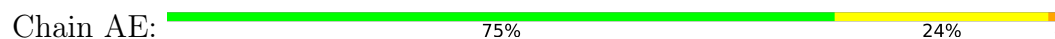
- Molecule 11: Ubiquitin-like protein FUBI



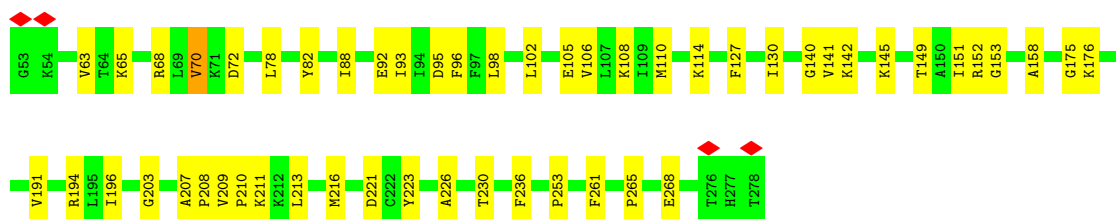
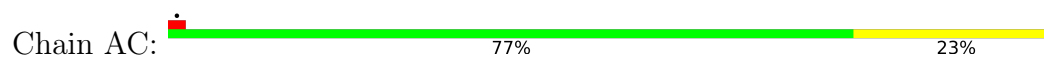
- Molecule 12: Small ribosomal subunit protein uS4



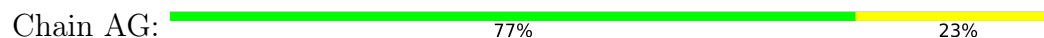
- Molecule 13: 40S ribosomal protein S4, X isoform

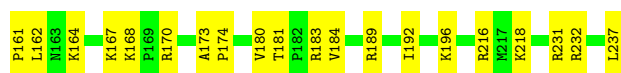


- Molecule 14: 40S ribosomal protein S2

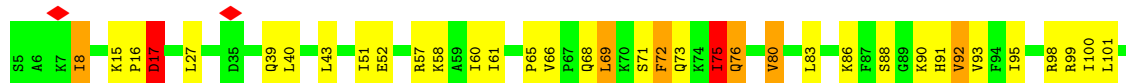


- Molecule 15: 40S ribosomal protein S6

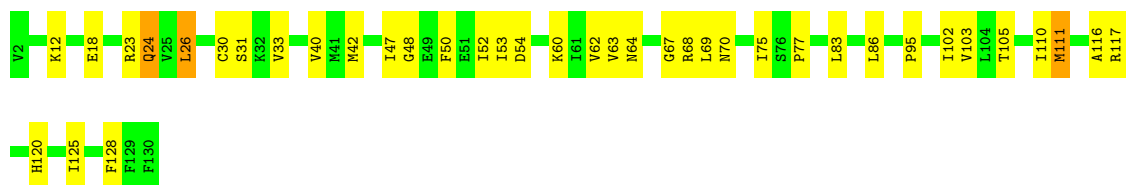




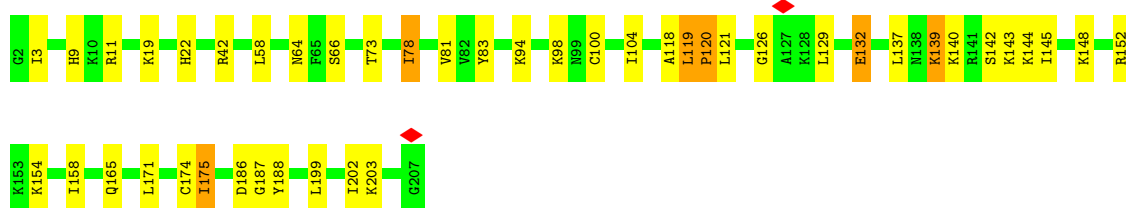
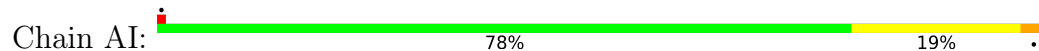
- Molecule 16: 40S ribosomal protein S7



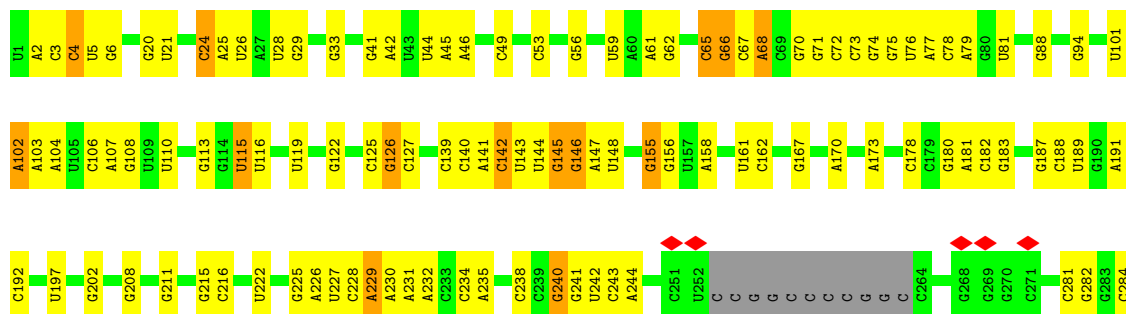
- Molecule 17: Small ribosomal subunit protein uS8



- Molecule 18: 40S ribosomal protein S8



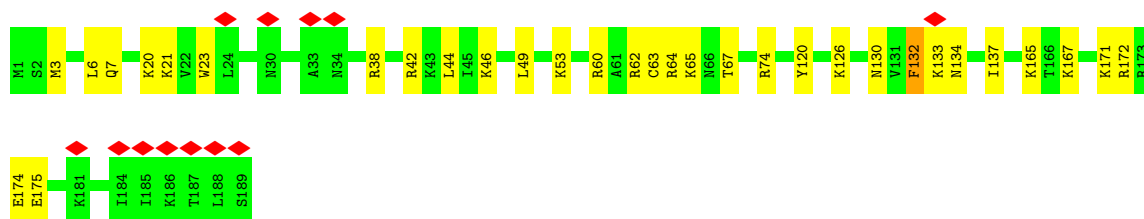
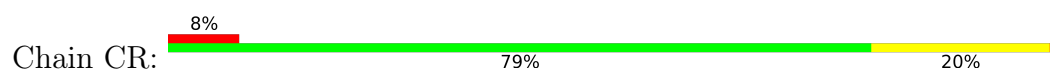
- Molecule 19: 18S ribosomal RNA



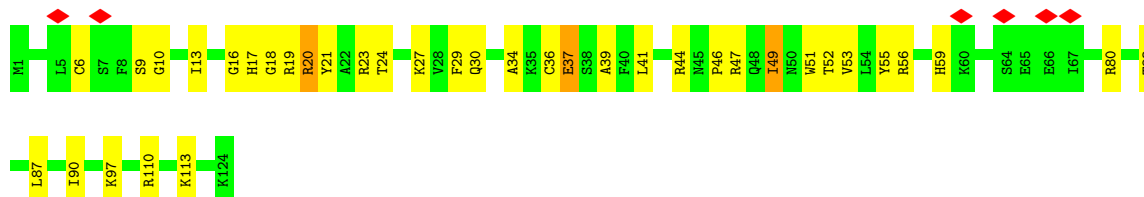
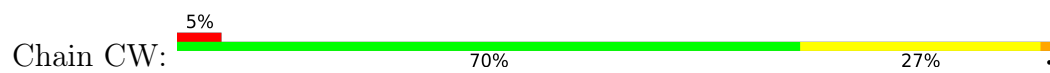
A1561	C1464	G1387	U1307	C1215	U1120	U1017	A920	C840	C753	A679	A590	G504	C382	U286
G1566	A1465	U1392	U1308	C1216	G1121	U1018	G923	G841	C757	G683	U591	G507	G383	U257
G1567	G1466	G1393	C1309	A1217	C1123	U1021	G924	U844	C	G684	C592	A508	U384	G288
G1570	A1474	G1394	U1310	C1218	C1124	A1022	G845	G846	U	A685	C593	G509	G385	G
G1571	A1476	C1395	G1311	G1221	G1125	A1023	A926	A847	C	A686	A594	G510	C293	U294
G1575	U1477	U1397	G1312	G1222	G1126	G1028	G927	U848	G	C687	G600	U511	C295	C296
G1576	A1489	A1401	A1313	G1223	C1127	U1029	G928	U849	A	U688	G601	A512	A302	A302
G1577	G1490	A1402	U1314	G1224	C1128	G1043	G929	A849	U	G689	G602	G513	C303	C303
U1578	U1403	G1316	U1315	G1225	G1129	U1044	C930	G852	G	G690	C603	C517	C304	C304
U1579	U1404	G1317	G1318	A1228	G1130	G1045	G933	G855	U	G691	A605	G518	U305	U305
A1580	G1495	U1319	G1320	G1229	G1131	U1045	G934	G855	C	A693	G606	A519	C306	C306
G1584	U1496	U1321	G1322	U1232	C1132	A1049	G935	G855	C	G694	U607	G407	G307	G307
U1585	U1497	U1323	G1324	G1233	U1136	A1050	U939	A861	U	C695	C608	A408	C308	C308
U1586	U1498	G1234	U1137	G1234	C1137	G1051	U940	G867	U	U524	U609	A409	G309	G309
U1587	G1500	G1235	C1138	G1235	U1139	A1052	C941	G872	A	A525	G610	G410	G312	G312
A1588	U1504	U1239	C1139	U1239	G1140	C1053	U943	A869	G	G611	G611	A526	G	G
G1593	U1505	A1240	G1140	A1240	G1141	A1060	A944	A870	U	U612	G613	A529	A318	A318
G1597	A1506	A1241	A1144	A1241	A1144	U1061	C948	A871	G	G	G614	U530	C319	C319
G1598	U1507	U1242	A1145	U1242	A1145	A1062	G949	A872	A	C	G615	A531	C322	C322
G1599	A1508	U1243	A1148	U1243	A1148	G1067	U954	A873	G	U	A616	A532	C323	C323
G1600	U1509	G1244	A1149	G1244	A1149	G1068	A955	A874	U	G	G617	A533	C324	C324
A1601	C1518	G1245	A1150	G1245	A1150	U1069	G956	C876	U	C	C618	G534	C325	C325
A1602	U1519	A1246	U1151	A1246	U1151	A1080	A957	C877	U	C	A628	G535	C326	C326
G1605	G1520	C1247	C1152	G1247	U1152	A1081	G958	C878	C	C	A629	A536	G330	G330
G1606	U1521	A1251	U1153	A1251	U1153	A1082	G961	C879	G	C	G634	G544	G331	G331
G1607	A1522	C1252	U1154	G1252	U1154	A1083	A962	U882	C	A	C639	G547	G332	G332
G1608	C1523	A1253	U1155	G1253	U1155	A1084	A962	U883	C	C	A640	C548	G333	G333
G1609	U1526	C1254	U1156	G1254	U1156	A1085	A969	C884	C	C	A641	C549	G334	G334
G1610	A1531	G1255	U1157	G1255	U1157	A1086	G970	C885	C	C	A642	U551	G335	G335
G1613	U1535	G1256	G1155	G1256	G1155	C1090	G971	A886	C	C	A643	U552	G336	G336
G1614	G1536	A1257	U1156	G1257	U1156	C1095	G982	U887	C	C	G644	U553	G337	G337
G1615	A1537	A1258	U1157	G1258	U1157	G1096	A983	U890	C	C	U649	A554	G338	G338
G1616	C1538	U1263	U1170	G1263	U1170	C1097	A983	U890	C	C	U650	A555	U345	U345
U1618	U1539	C1264	G1171	G1264	G1171	C1098	A990	U891	C	C	A651	U556	C346	C346
A1620	G1540	A1265	U1172	G1265	U1172	C1099	A991	G894	C	C	U652	U557	G347	G347
A1621	U1541	C1266	A1173	G1266	A1173	A1100	A992	G895	C	C	U653	U558	A348	A348
A1622	G1542	G1267	U1183	G1267	U1183	A1101	A992	G895	C	C	A654	G559	A349	A349
A1623	C1543	U1272	U1184	G1272	U1184	A1102	G999	U900	C	C	U655	A560	C350	C350
U1631	U1544	C1273	U1193	G1273	U1193	C1103	C1000	G901	C	C	A656	A561	G351	G351
U1632	G1545	G1274	U1194	G1274	U1194	C1104	A1001	G902	C	C	U657	U562	C352	C352
U1633	U1546	G1275	A1195	G1275	A1195	C1105	U1004	G903	C	C	C660	A564	U368	U368
U1634	U1549	A1284	U1202	G1284	U1202	C1106	G1005	A903	C	C	U666	C568	C369	C369
U1637	G1550	U1285	G1203	G1285	G1203	C1107	A1008	G909	C	C	U667	U742	G370	G370
G1638	U1551	G1286	A1204	G1286	A1204	C1108	U1009	G910	C	C	U668	U743	A371	A371
U1643	C1552	A1287	C1205	G1287	C1205	U1109	G1010	G911	C	C	A493	A574	U372	U372
U1648	U1553	U1288	G1206	G1288	G1206	U1110	A1011	A913	C	C	A494	A575	G373	G373
U1649	A1556	A1301	G1207	G1288	G1207	U1111	A1012	U914	C	C	A495	U577	G374	G374
	C1557	A1302	A1208	G1289	A1208	U1112	U1013	G915	C	C	A496	U577	U375	U375
	U1462	G1302	A1209	G1290	A1209	U1115	U1014	G916	C	C	A500	U582	A376	A376
	U1463	C1303	G1211	G1291	G1211	U1116	U1015	U917	C	C	C501	U583	G377	G377
			U1212	G1292	U1212	U1117	U1016	U918	C	C	C502	G588	C381	C381
						U1119		A919	C	C	U678	G589		



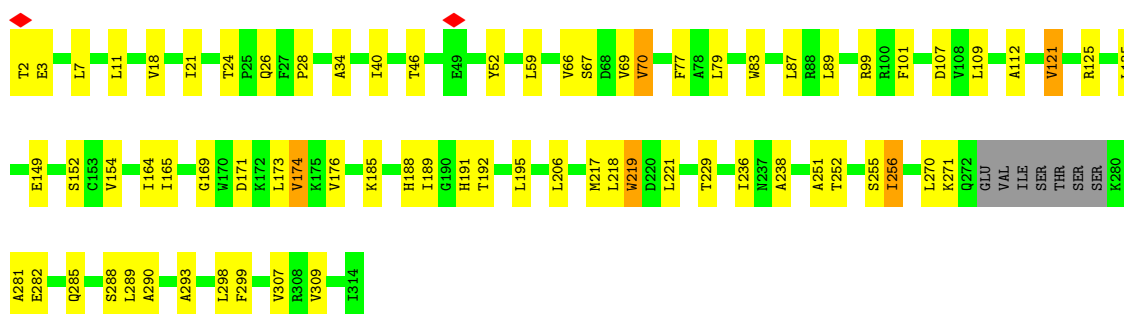
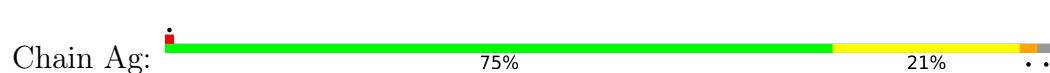
• Molecule 20: 60S ribosomal protein L19



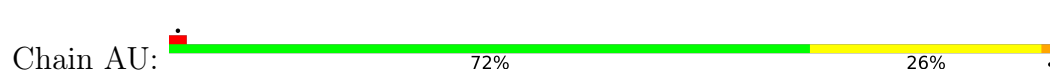
• Molecule 21: Large ribosomal subunit protein eL24



• Molecule 22: Small ribosomal subunit protein RACK1



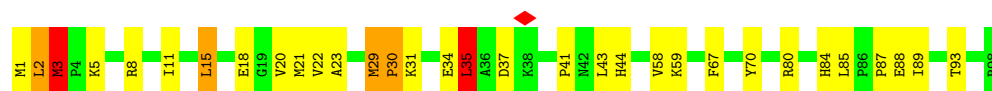
• Molecule 23: 40S ribosomal protein S20



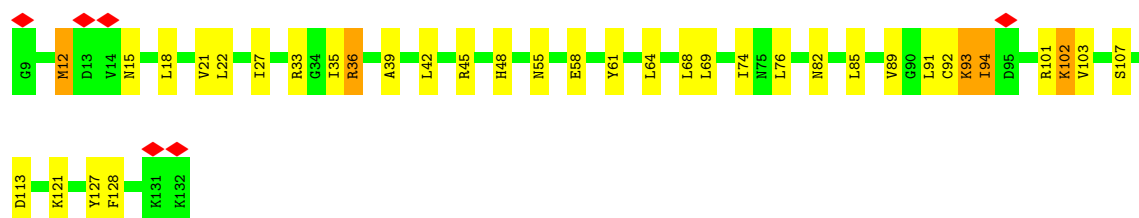
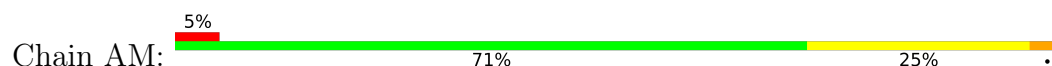




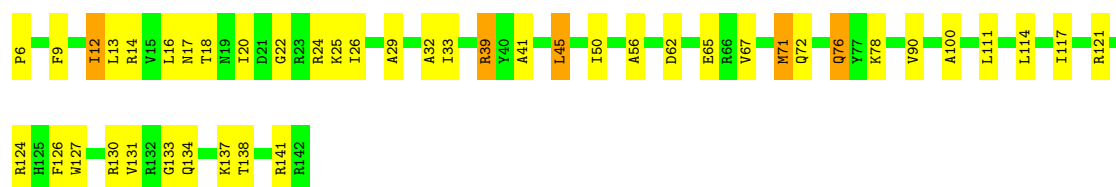
- Molecule 24: Small ribosomal subunit protein eS10



- Molecule 25: 40S ribosomal protein S12



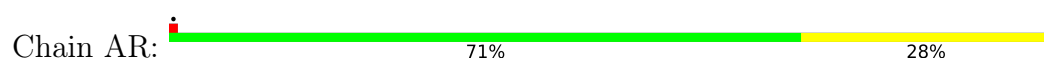
- Molecule 26: Small ribosomal subunit protein uS13



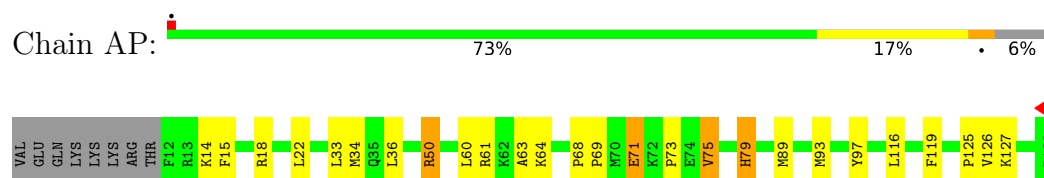
- Molecule 27: Small ribosomal subunit protein uS14



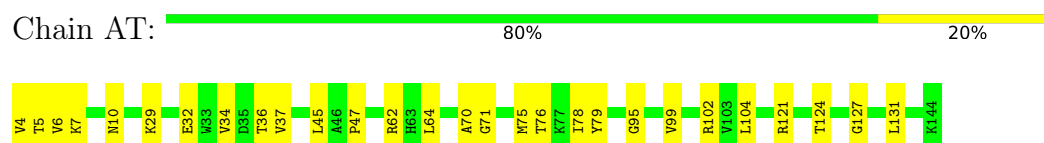
- Molecule 28: Small ribosomal subunit protein eS17



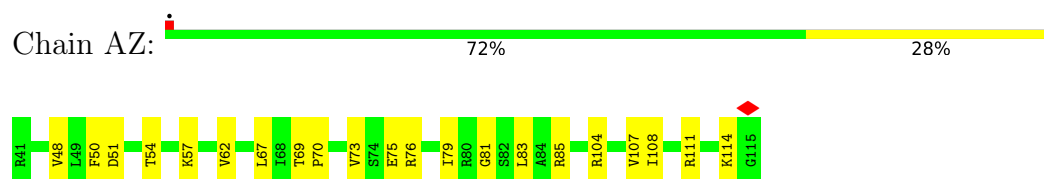
- Molecule 29: 40S ribosomal protein S15



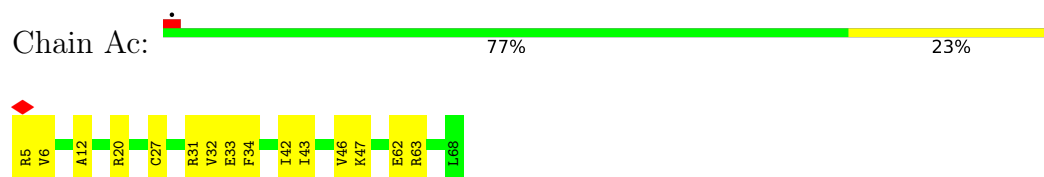
- Molecule 30: Small ribosomal subunit protein eS19



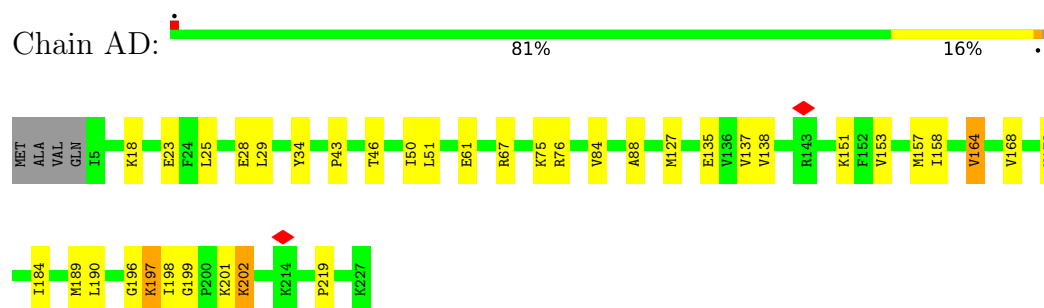
- Molecule 31: 40S ribosomal protein S25



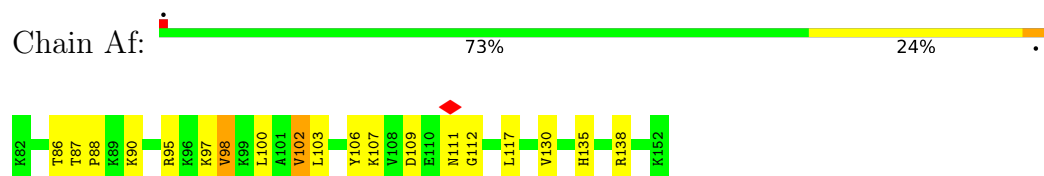
- Molecule 32: 40S ribosomal protein S28




- Molecule 33: 40S ribosomal protein S3

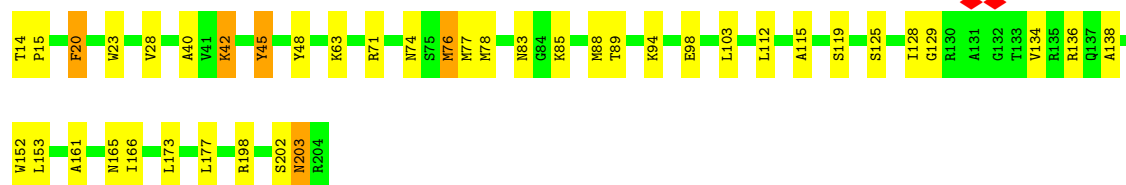


- Molecule 34: Ubiquitin-ribosomal protein eS31 fusion protein




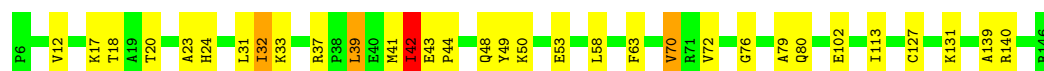
- Molecule 35: Small ribosomal subunit protein uS7

Chain AF:  79% 19%



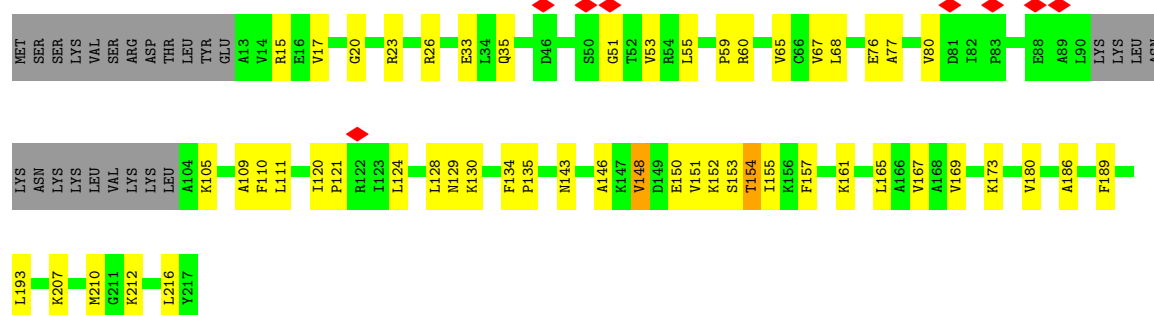
- Molecule 36: Small ribosomal subunit protein uS9

Chain AQ:  77% 20%




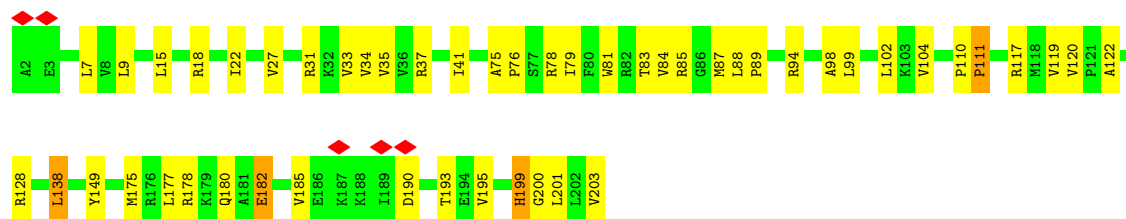
- Molecule 37: 60S ribosomal protein L10a

Chain Cz:  64% 24% 12%




- Molecule 38: 60S ribosomal protein L13a

Chain CO:  75% 23%



- Molecule 39: 60S ribosomal protein L13

Chain CL:  80% 18%





- Molecule 40: Large ribosomal subunit protein uL14

Chain CV: 86% 12%



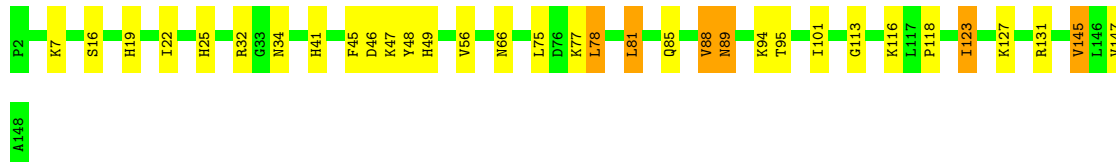
- Molecule 41: 60S ribosomal protein L14

Chain CM: 69% 30%



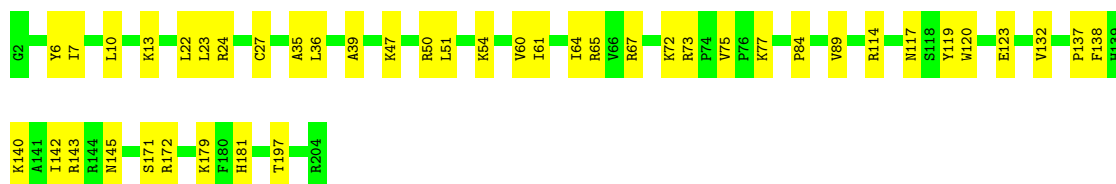
- Molecule 42: 60S ribosomal protein L27a

Chain Ca: 78% 18%



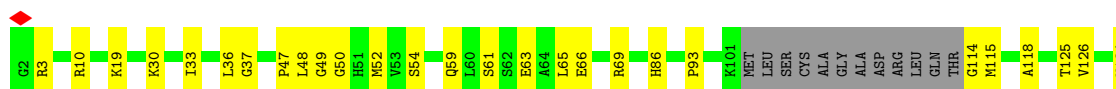
- Molecule 43: Ribosomal protein L15

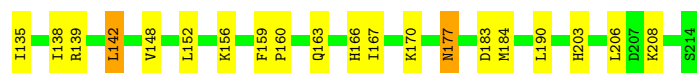
Chain CN: 79% 21%



- Molecule 44: 60S ribosomal protein L10-like

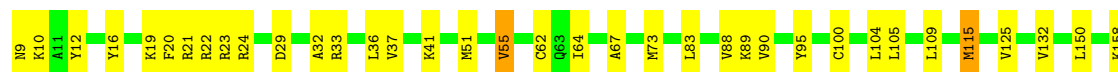
Chain CI: 72% 21% 6%





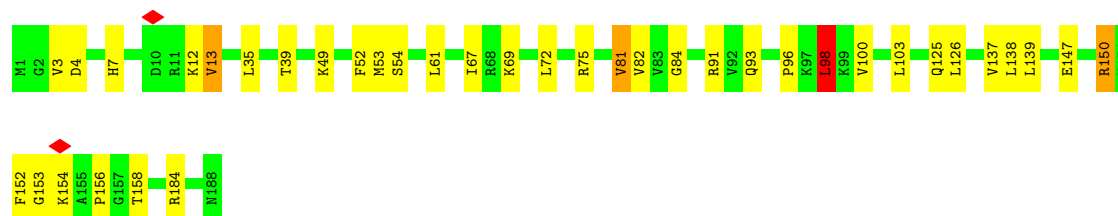
- Molecule 45: 60S ribosomal protein L5

Chain CD: 78% 21% .



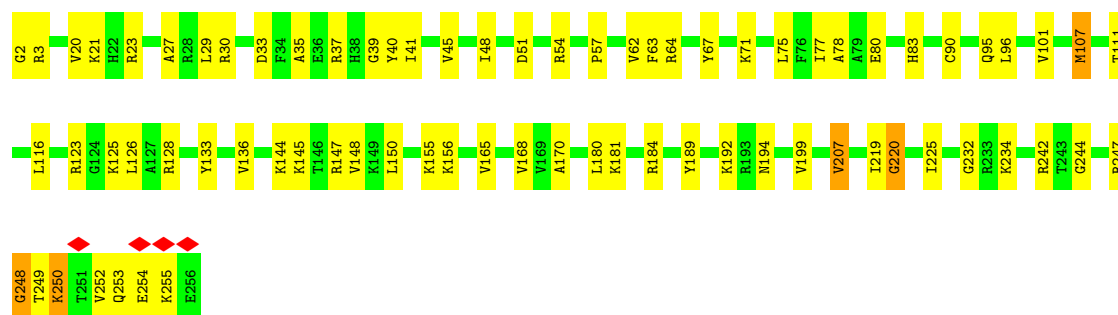
- Molecule 46: 60S ribosomal protein L18

Chain CQ: 80% 18% ..



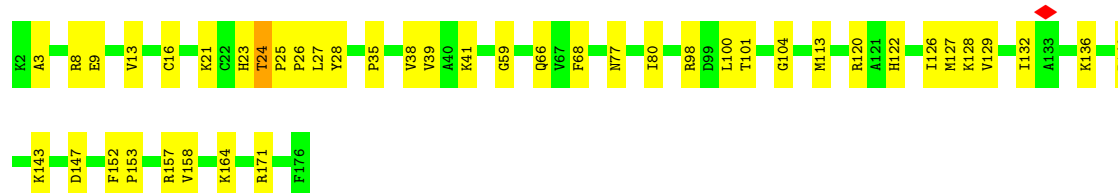
- Molecule 47: Large ribosomal subunit protein uL2

Chain CA: 71% 27% .

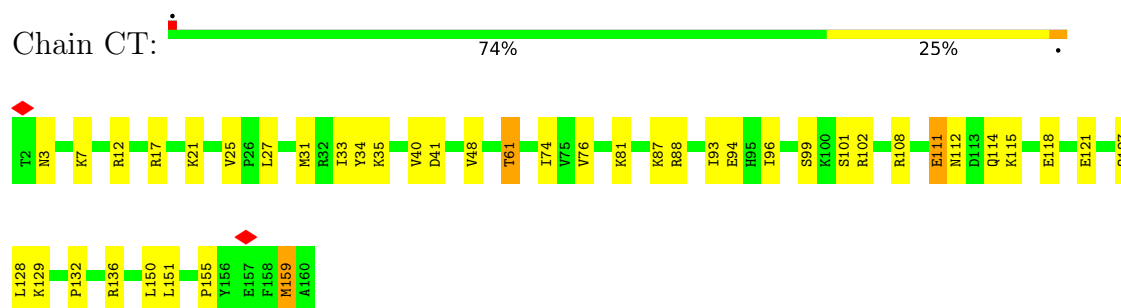


- Molecule 48: 60S ribosomal protein L18a

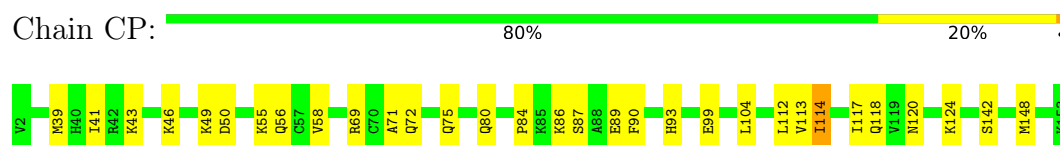
Chain CS: 75% 24% .



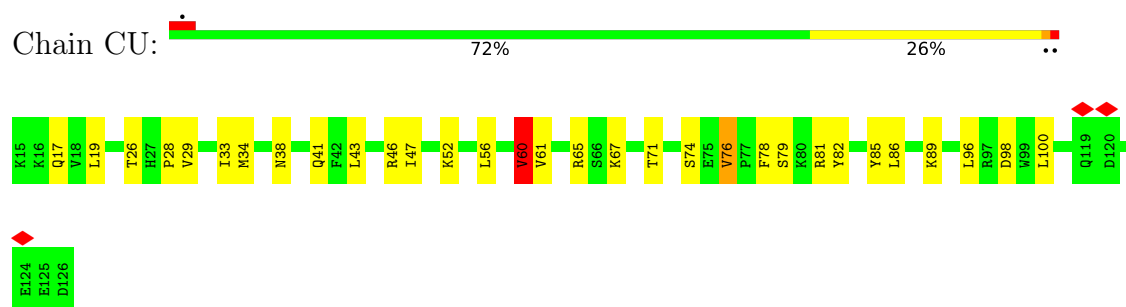
- Molecule 49: Large ribosomal subunit protein eL21



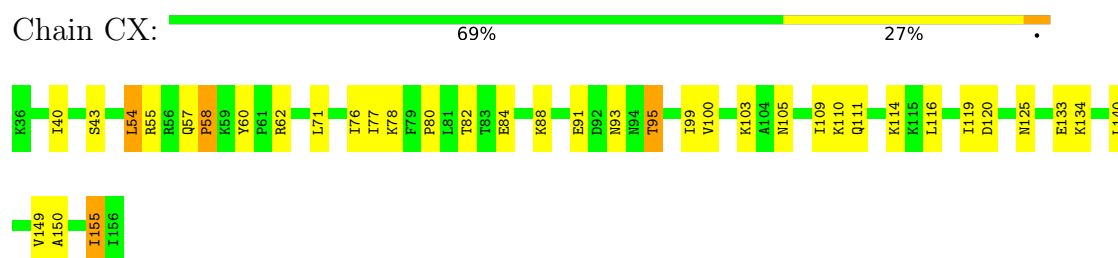
- Molecule 50: 60S ribosomal protein L17



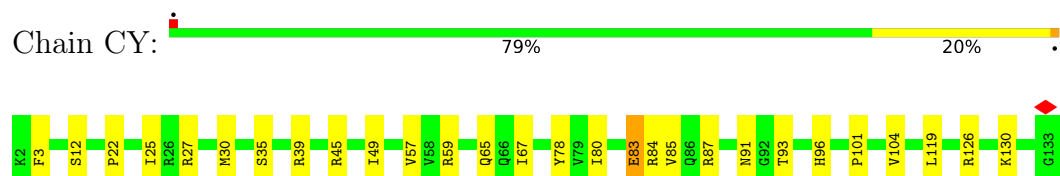
- Molecule 51: Large ribosomal subunit protein eL22



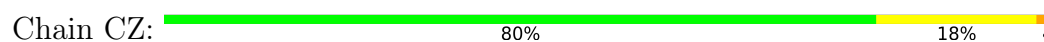
- Molecule 52: Large ribosomal subunit protein uL23



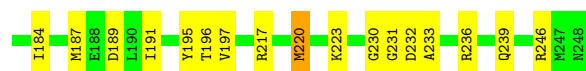
- Molecule 53: 60S ribosomal protein L26



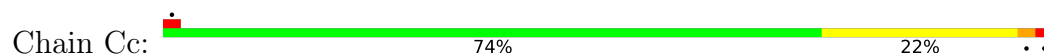
- Molecule 54: 60S ribosomal protein L27



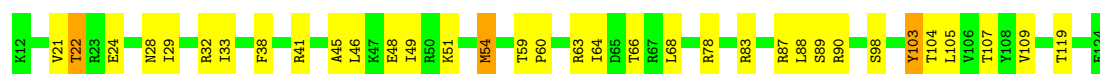




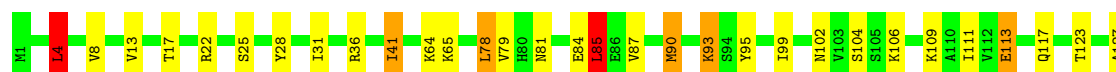
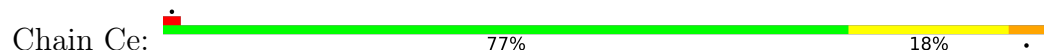
- Molecule 60: 60S ribosomal protein L30



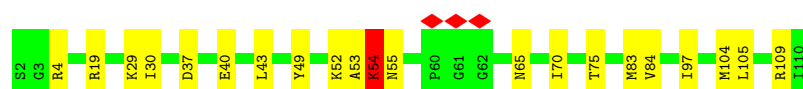
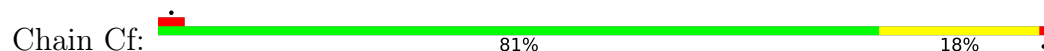
- Molecule 61: Large ribosomal subunit protein eL31



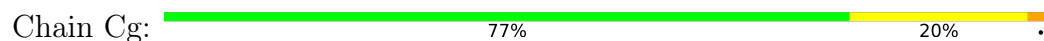
- Molecule 62: 60S ribosomal protein L32



- Molecule 63: 60S ribosomal protein L35a



- Molecule 64: Large ribosomal subunit protein eL34




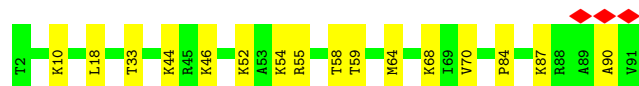
- Molecule 65: 60S ribosomal protein L36





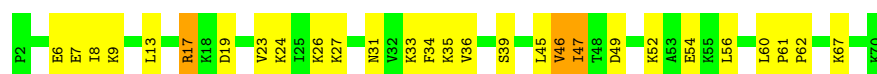
- Molecule 66: Ribosomal protein L37

Chain Cj:  82% 18%




- Molecule 67: Large ribosomal subunit protein eL38

Chain Ck:  59% 36%



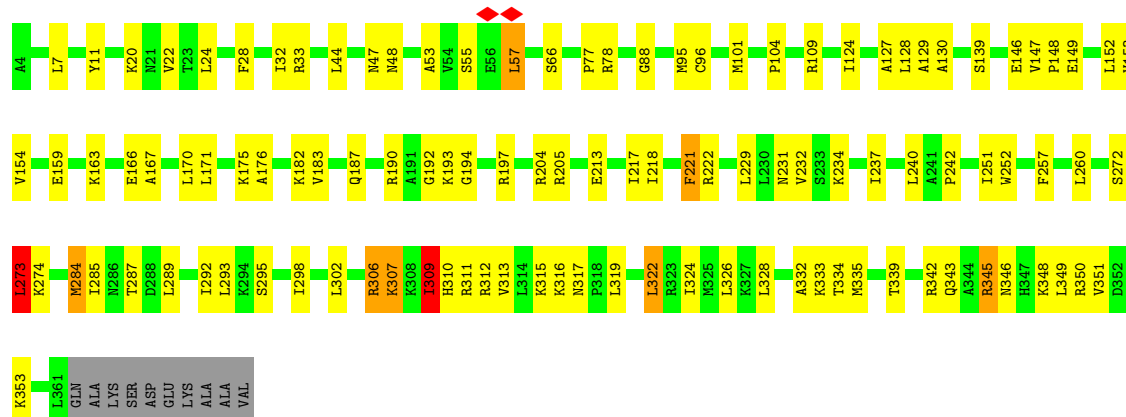
- Molecule 68: Large ribosomal subunit protein eL39

Chain Cl:  78% 22%



- Molecule 69: 60S ribosomal protein L4

Chain CC:  67% 28%



- Molecule 70: Ubiquitin-ribosomal protein eL40 fusion protein

Chain Cm:  71% 27%

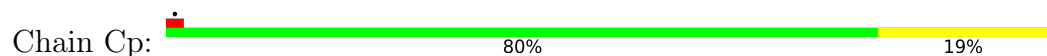


- Molecule 71: 60S ribosomal protein L41

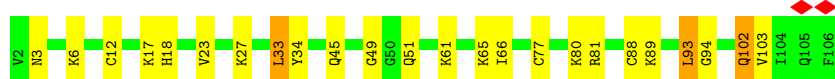
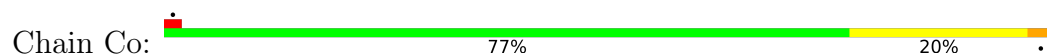
Chain Cn:  72% 24%



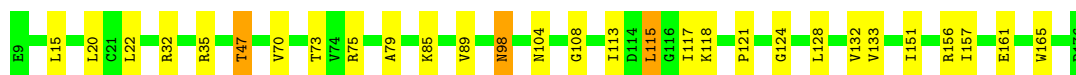
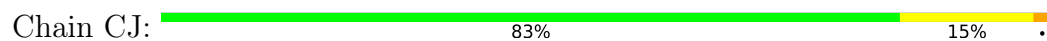
- Molecule 72: Large ribosomal subunit protein eL43



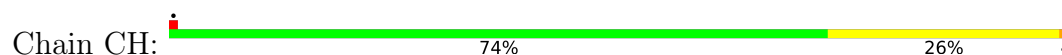
- Molecule 73: 60S ribosomal protein L36a



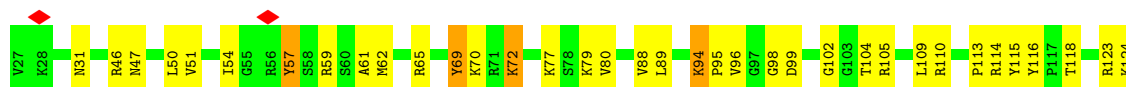
- Molecule 74: Large ribosomal subunit protein uL5



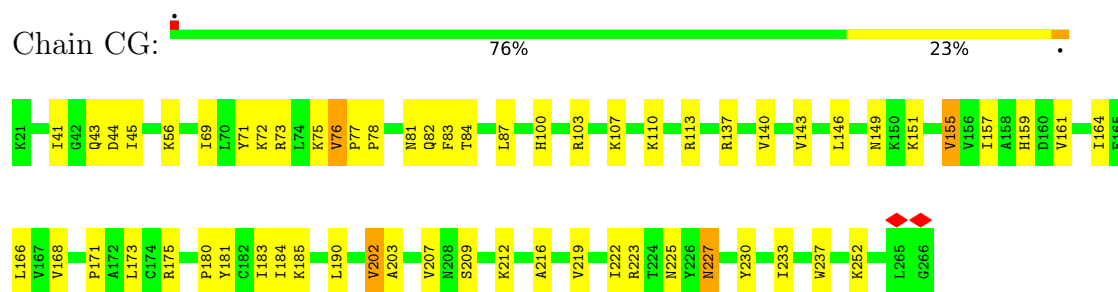
- Molecule 75: 60S ribosomal protein L9



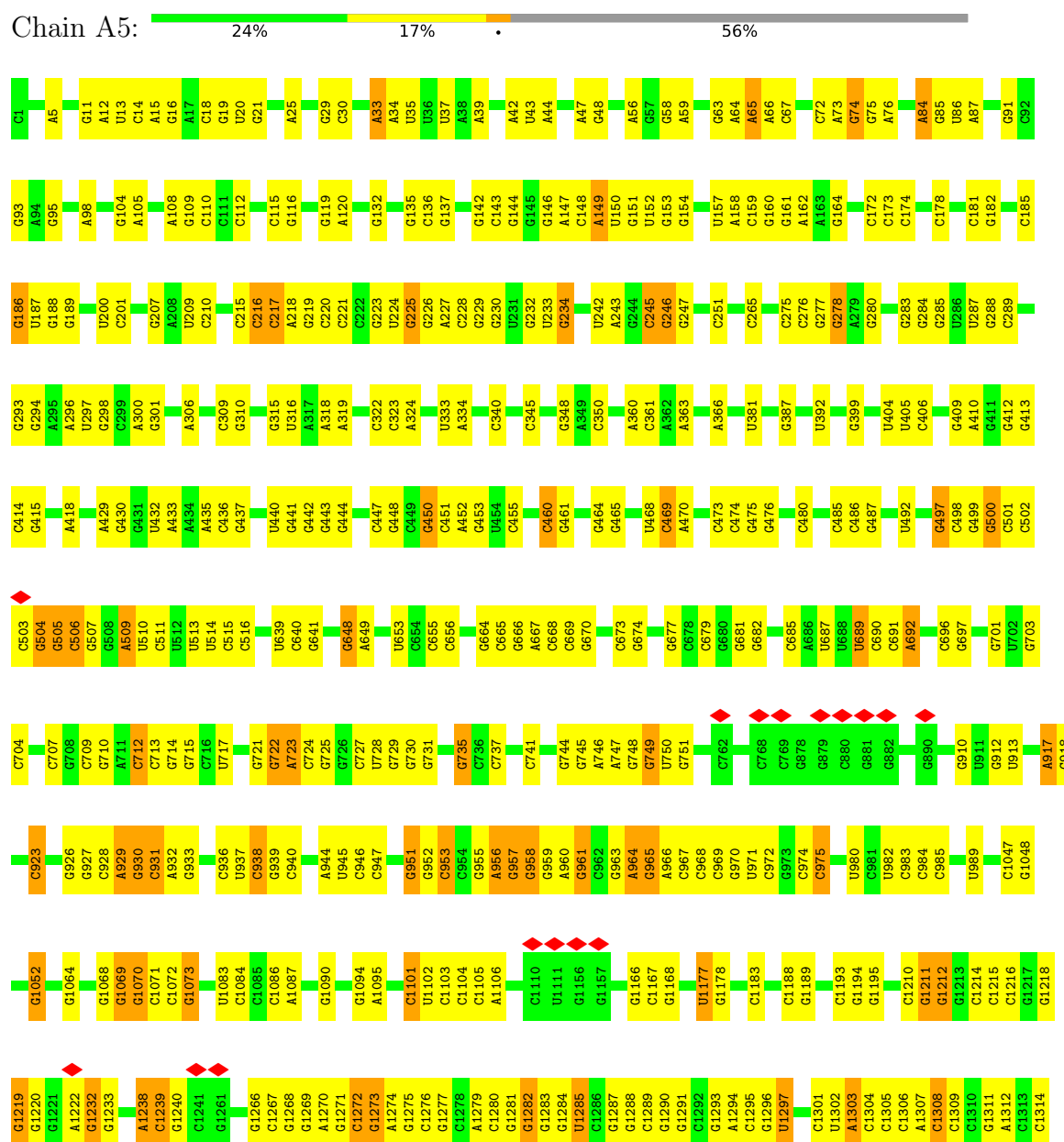
- Molecule 76: 60S ribosomal protein L6



• Molecule 77: 60S ribosomal protein L7a



• Molecule 78: 28S ribosomal RNA





C A A U G U A G G U A A G G G A A G U C G G C A A G C C G G A U C C G U A A C U U C G G A U A A G G A U C U D

A A G G C U G G G U C G G U C C G G G C U G G G G C G G C G G A A G C G G G C U D G G G C C G C G C G A G C C G G

G C C C U U C C C G G U G G A U C C G C C C A G C C U G C G G C G G G G G C G C C U C G G C C G G G C C U U A

G C A G C C G A C C U U A A A C C U G G U G C C G G G A C C A C U G G U U A

U C G C G A A G G C C C G G C G G G G U G G A C C G C G A A U G U G A U D C C A G U U G C C U C U G A A U D G U C

A A A G U A A G A A A A U U C A A A U G A A G C C G G U A A C C G G U A A C G G A A C U A U G A C U C U C U A A G

G U A G C C A A A U G C U C G G U C A U C U A A U A G A C G C G C A U G A A A U G A C G A A G A A U C C C A

C U G U C C C U A C C U A C U A U C C A G C C A A C C A C A C C A A G G G A A C C U U G G C C G G A A U C A G C

G G G A A A A G A A A C C U U G U G A G C C U G A C C U C C U A G C C A C C A C C U G G C A A C A A G G G

U G U A A A A A A G U G G A A G C C C C G G C G G C C C C C C C G G C C C G G G G G C C G G C G C G C

G G U G A A A U A C C U A C C U U C U G A U C C G G U U U C A C U G A C C C G G G G G A G C C G G G G C C

C C G A G G G G C C U C U G G U U C U G G C C G G C C A A G C C C C G G G C C C C C C C C C C C C C C C C

C U C C G G G A C A U G C C A G G U G G G A G A U U U G U G C C G G G U A C C C C C C C C C C C C C C C C

G C A G G U C U C C U A A G G C G A A A C C U C

A G C U C G C U U C U A U U U C U U G A

C U U C U G A C C U U U G G G U U U A A A G C A G G A G G U C C A G G A A A A A A A A A A A A A A A A A A A

C U U G U G C C A A G C C C C A A G C C G U U C A A G C C A A G C C G U U U A A C C C C C C C C C C C C C C C

C U A U C A U U G U G A A G C A A G A A U U C C A A G C C A A G C

G A G C U G G G U U U A G A C C C G U C G U G A A G A C A G G G U U A C

C C A U G G U A A C C U G C C U C C A A G C C A A G G A A C C G C A A G G U U C C A A C C C C C C C C C C C C

U G G C U G A A G G A G C C A U C G G G G G G A A G C A C C A U G G G A A C C C C C C C C C C C C C C C C C

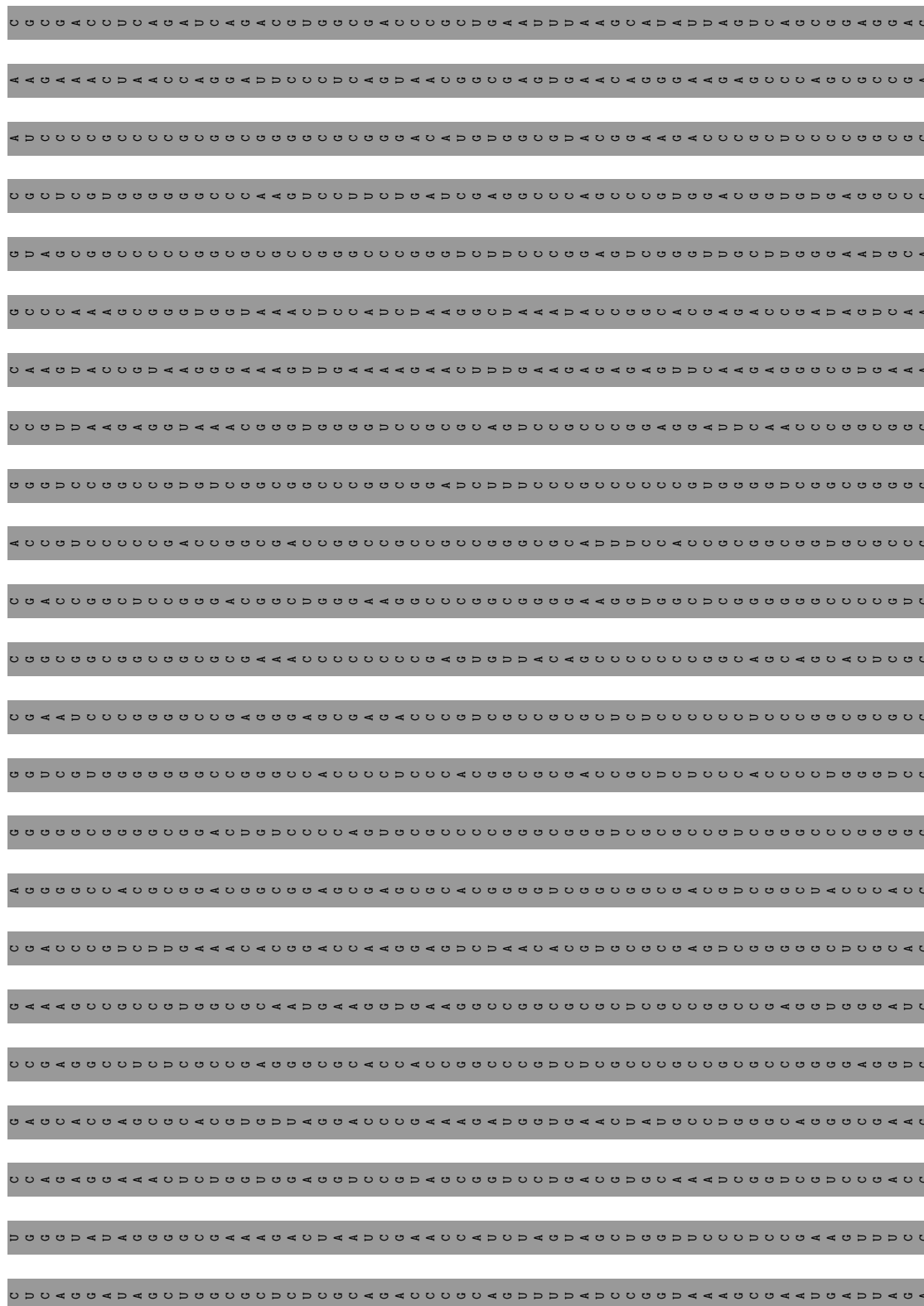
G U C A A A U C C C G C C C A A G C C G A U A C C G C A G C C G G G G C C C C C C C C C C C C C C C C C C

A U A G C C G U C C C C G C

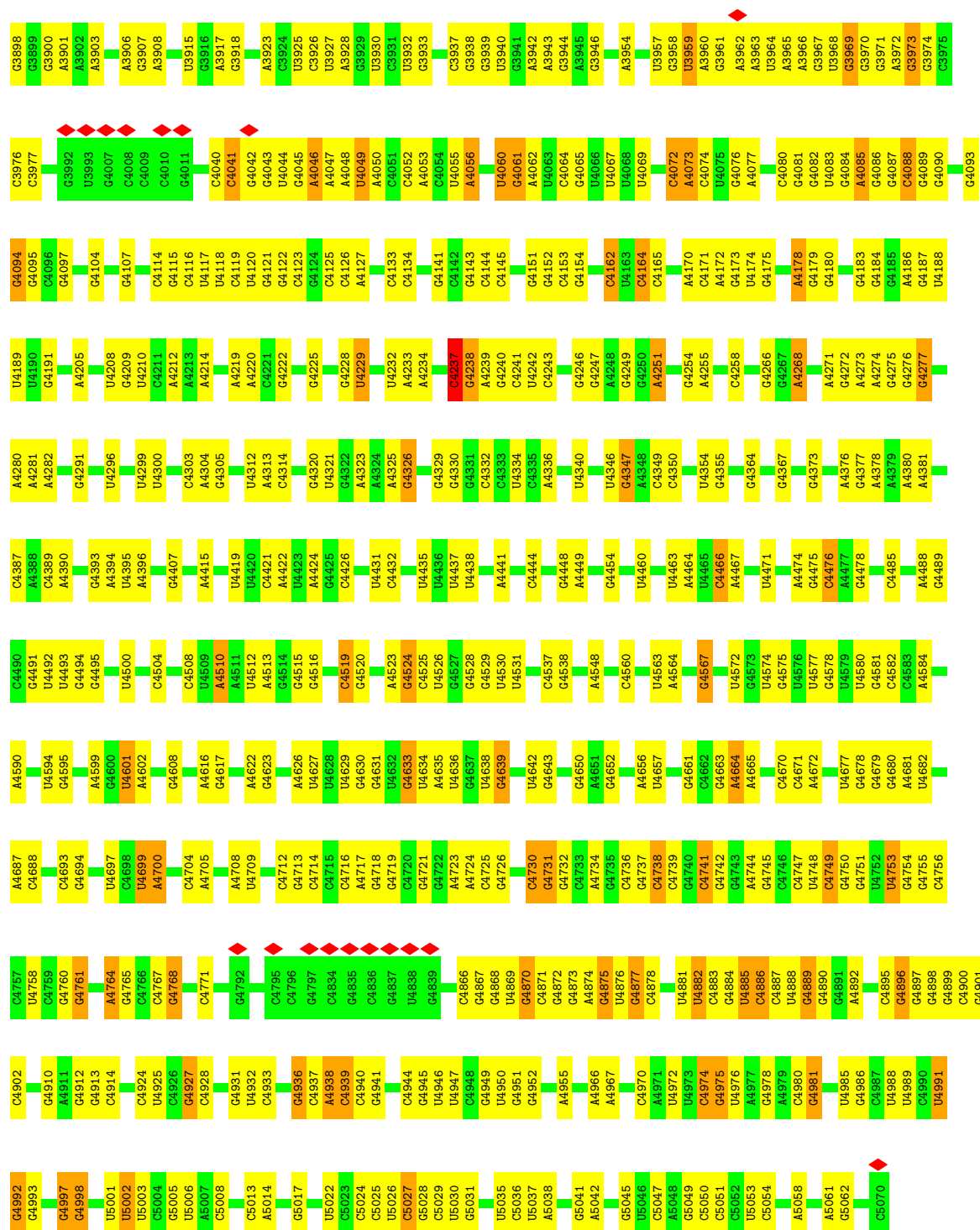
C C G G G U C C G G G C G G G A C

C G C C C C C U C C G C C C G U C C A C C C C G C A C G U U C C G U G G G A A C C C C C C C C C C C C C C C C

G A C G A C C U G G U G G U G











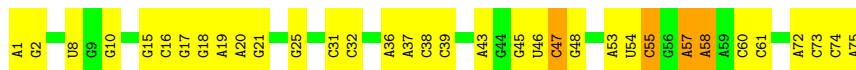
- Molecule 80: 5.8S ribosomal RNA

Chain A8: 61% 36%



- Molecule 81: E-tRNA

Chain BC: 55% 40% 5%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86927	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	AO	0.30	0/1029	0.81	1/1380 (0.1%)
2	AX	0.32	0/1124	0.76	0/1500
3	AN	0.33	0/1232	0.83	2/1656 (0.1%)
4	AL	0.34	0/1319	0.90	5/1761 (0.3%)
5	AB	0.32	0/1774	0.86	1/2372 (0.0%)
6	AA	0.32	0/1679	0.77	3/2283 (0.1%)
7	AV	0.35	0/631	0.92	1/844 (0.1%)
8	AY	0.32	0/1040	0.89	5/1382 (0.4%)
9	Aa	0.28	0/863	0.80	2/1159 (0.2%)
10	Ab	0.39	0/673	0.94	5/902 (0.6%)
11	Ae	0.32	0/474	0.79	0/623
12	AJ	0.34	0/1487	0.83	3/1985 (0.2%)
13	AE	0.30	0/2126	0.77	3/2859 (0.1%)
14	AC	0.32	0/1788	0.81	5/2414 (0.2%)
15	AG	0.25	0/1946	0.63	1/2590 (0.0%)
16	AH	0.37	0/1553	0.95	9/2079 (0.4%)
17	AW	0.31	0/1051	0.77	1/1406 (0.1%)
18	AI	0.30	0/1715	0.86	8/2287 (0.3%)
19	B2	0.97	13/42229 (0.0%)	0.44	14/65756 (0.0%)
20	CR	0.31	0/1267	0.83	3/1672 (0.2%)
21	CW	0.34	0/1030	0.82	0/1364
22	Ag	0.24	0/2443	0.65	3/3324 (0.1%)
23	AU	0.32	0/832	0.84	1/1117 (0.1%)
24	AK	0.40	0/851	1.10	8/1147 (0.7%)
25	AM	0.34	0/970	0.88	5/1300 (0.4%)
26	AS	0.31	0/1157	0.86	9/1548 (0.6%)
27	Ad	0.23	0/455	0.74	0/603
28	AR	0.39	0/1031	0.96	2/1383 (0.1%)
29	AP	0.35	0/1011	0.95	6/1349 (0.4%)
30	AT	0.27	0/1119	0.66	1/1499 (0.1%)
31	AZ	0.24	0/604	0.66	2/810 (0.2%)
32	Ac	0.27	0/508	0.90	3/680 (0.4%)
33	AD	0.31	0/1764	0.84	10/2375 (0.4%)
34	Af	0.37	0/593	0.90	1/786 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	AF	0.33	0/1531	0.83	3/2059 (0.1%)
36	AQ	0.26	0/1142	0.81	3/1528 (0.2%)
37	Cz	0.32	1/1560 (0.1%)	0.70	1/2095 (0.0%)
38	CO	0.35	0/1687	0.82	4/2257 (0.2%)
39	CL	0.29	0/1732	0.72	0/2315
40	CV	0.28	0/1003	0.85	1/1345 (0.1%)
41	CM	0.31	0/1161	0.87	4/1552 (0.3%)
42	Ca	0.30	0/1191	0.82	2/1591 (0.1%)
43	CN	0.30	0/1746	0.73	1/2338 (0.0%)
44	CI	0.34	0/1665	0.76	1/2223 (0.0%)
45	CD	0.28	0/2398	0.76	4/3210 (0.1%)
46	CQ	0.31	0/1545	0.80	4/2062 (0.2%)
47	CA	0.82	1/1995 (0.1%)	0.86	7/2674 (0.3%)
48	CS	0.34	0/1493	0.86	5/2003 (0.2%)
49	CT	0.29	0/1326	0.84	5/1770 (0.3%)
50	CP	0.33	0/1259	0.80	2/1689 (0.1%)
51	CU	0.34	0/935	0.93	3/1253 (0.2%)
52	CX	0.33	0/1011	0.93	4/1356 (0.3%)
53	CY	0.35	0/1124	0.89	4/1494 (0.3%)
54	CZ	0.34	1/1130 (0.1%)	0.79	1/1507 (0.1%)
55	Cr	0.44	0/1120	1.10	8/1497 (0.5%)
56	Ch	0.36	0/1031	0.92	5/1361 (0.4%)
57	Cb	0.42	1/564 (0.2%)	0.90	2/743 (0.3%)
58	CB	0.31	0/3229	0.80	7/4323 (0.2%)
59	CF	0.31	0/1945	0.82	2/2589 (0.1%)
60	Cc	0.39	0/787	0.98	5/1057 (0.5%)
61	Cd	0.31	0/946	0.83	1/1272 (0.1%)
62	Ce	0.38	1/1114 (0.1%)	0.82	5/1485 (0.3%)
63	Cf	0.33	0/895	0.89	2/1198 (0.2%)
64	Cg	0.28	0/916	0.78	0/1220
65	Ci	0.38	0/851	0.95	4/1125 (0.4%)
66	Cj	0.22	0/748	0.60	0/990
67	Ck	0.33	0/575	0.93	5/761 (0.7%)
68	Cl	0.25	0/454	0.65	0/599
69	CC	0.31	0/2907	0.84	6/3905 (0.2%)
70	Cm	0.32	0/435	0.84	1/575 (0.2%)
71	Cn	0.29	0/241	0.79	0/305
72	Cp	0.28	0/713	0.74	0/946
73	Co	0.30	0/877	0.82	1/1156 (0.1%)
74	CJ	0.31	0/1372	0.80	1/1836 (0.1%)
75	CH	0.29	0/1545	0.80	1/2077 (0.0%)
76	CE	0.33	0/2153	0.90	7/2878 (0.2%)
77	CG	0.31	0/2006	0.76	0/2697

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	A5	0.20	0/40489	0.45	12/63083 (0.0%)
78	A6	0.19	0/49259	0.43	10/76579 (0.0%)
79	A7	0.17	0/2880	0.33	0/4489
80	A8	0.18	0/3723	0.40	1/5800 (0.0%)
81	BC	0.16	0/1795	0.35	0/2798
All	All	0.48	18/235572 (0.0%)	0.61	268/345860 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AO	0	1
2	AX	0	1
6	AA	0	1
11	Ae	0	1
12	AJ	0	1
14	AC	0	1
16	AH	0	2
17	AW	0	1
18	AI	0	3
20	CR	0	1
21	CW	0	1
24	AK	0	1
25	AM	0	1
28	AR	0	1
29	AP	0	2
30	AT	0	1
34	Af	0	1
35	AF	0	2
36	AQ	0	1
38	CO	0	2
39	CL	0	1
42	Ca	0	1
44	CI	0	1
45	CD	0	1
46	CQ	0	2
47	CA	0	3
48	CS	0	1
49	CT	0	2
52	CX	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
55	Cr	0	5
58	CB	0	1
60	Cc	0	1
61	Cd	0	1
63	Cf	0	1
69	CC	0	3
73	Co	0	2
75	CH	0	1
76	CE	0	2
77	CG	0	1
All	All	0	57

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	B2	1207	G	C5'-C4'	103.83	3.58	1.51
19	B2	1044	G	C6-N1	60.35	2.60	1.39
19	B2	1044	G	N3-C4	57.34	2.50	1.35
19	B2	1044	G	C2-N3	56.62	2.46	1.32
19	B2	1044	G	N1-C2	56.59	2.50	1.37

The worst 5 of 268 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	CA	248	GLY	O-C-N	-14.20	104.24	122.70
19	B2	1207	G	C5'-C4'-C3'	11.51	139.02	116.00
32	Ac	62	GLU	CA-C-N	9.57	139.81	121.54
32	Ac	62	GLU	C-N-CA	9.57	139.81	121.54
47	CA	248	GLY	N-CA-C	9.20	134.97	113.18

There are no chirality outliers.

5 of 57 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AA	191	ARG	Peptide
12	AJ	172	ARG	Sidechain
1	AO	136	PRO	Peptide
2	AX	87	ASN	Peptide
11	Ae	46	VAL	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AO	1016	0	1039	24	0
2	AX	1106	0	1179	15	0
3	AN	1208	0	1294	21	0
4	AL	1296	0	1374	16	0
5	AB	1747	0	1829	31	0
6	AA	1642	0	1646	31	0
7	AV	625	0	628	15	0
8	AY	1023	0	1090	26	0
9	Aa	847	0	897	18	0
10	Ab	659	0	683	7	0
11	Ae	468	0	519	7	0
12	AJ	1463	0	1578	19	0
13	AE	2084	0	2189	38	0
14	AC	1751	0	1835	28	0
15	AG	1923	0	2089	41	0
16	AH	1530	0	1627	23	0
17	AW	1034	0	1080	24	0
18	AI	1686	0	1772	19	0
19	B2	37803	0	19015	344	0
20	CR	1257	0	1392	21	0
21	CW	1015	0	1079	26	0
22	Ag	2387	0	2344	41	0
23	AU	822	0	887	16	0
24	AK	827	0	854	15	0
25	AM	960	0	989	16	0
26	AS	1139	0	1191	23	0
27	Ad	445	0	442	4	0
28	AR	1019	0	1075	20	0
29	AP	992	0	1039	9	0
30	AT	1101	0	1135	15	0
31	AZ	598	0	656	10	0
32	Ac	506	0	536	8	0
33	AD	1736	0	1831	23	0
34	Af	581	0	599	10	0
35	AF	1509	0	1563	24	0
36	AQ	1124	0	1193	18	0
37	Cz	1534	0	1609	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	CO	1655	0	1799	34	0
39	CL	1701	0	1818	30	0
40	CV	989	0	1047	11	0
41	CM	1139	0	1209	24	0
42	Ca	1162	0	1213	22	0
43	CN	1701	0	1749	29	0
44	CI	1626	0	1662	22	0
45	CD	2353	0	2372	40	0
46	CQ	1521	0	1640	20	0
47	CA	1957	0	2055	69	0
48	CS	1453	0	1490	26	0
49	CT	1298	0	1366	26	0
50	CP	1233	0	1263	14	0
51	CU	921	0	928	17	0
52	CX	994	0	1079	22	0
53	CY	1107	0	1193	14	0
54	CZ	1107	0	1182	19	0
55	Cr	1104	0	1189	29	0
56	Ch	1023	0	1160	16	0
57	Cb	554	0	585	4	0
58	CB	3161	0	3297	50	0
59	CF	1910	0	2048	29	0
60	Cc	776	0	812	17	0
61	Cd	931	0	980	14	0
62	Ce	1096	0	1189	22	0
63	Cf	876	0	912	11	0
64	Cg	906	0	999	17	0
65	Ci	840	0	929	18	0
66	Cj	733	0	773	10	0
67	Ck	569	0	637	18	0
68	Cl	444	0	483	6	0
69	CC	2853	0	3028	69	0
70	Cm	429	0	469	9	0
71	Cn	240	0	289	5	0
72	Cp	703	0	755	11	0
73	Co	863	0	931	11	0
74	CJ	1349	0	1383	15	0
75	CH	1526	0	1605	28	0
76	CE	2113	0	2320	41	0
77	CG	1973	0	2128	41	0
78	A5	36244	0	18266	281	0
78	A6	44180	0	21937	334	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	A7	2578	0	1306	18	0
80	A8	3334	0	1693	18	0
81	BC	1604	0	816	15	0
All	All	219292	0	161761	2305	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 2305 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1834:A:C4	19:B2:1834:A:C5	2.07	1.39
47:CA:248:GLY:CA	47:CA:248:GLY:C	1.99	1.35
19:B2:1834:A:C5	19:B2:1834:A:C6	2.16	1.34
19:B2:1834:A:N3	19:B2:1834:A:C2	2.12	1.17
19:B2:1834:A:C2	19:B2:1834:A:N1	2.13	1.16

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AO	134/136 (98%)	115 (86%)	18 (13%)	1 (1%)	18	49
2	AX	140/142 (99%)	129 (92%)	11 (8%)	0	100	100
3	AN	148/150 (99%)	136 (92%)	10 (7%)	2 (1%)	9	34
4	AL	156/158 (99%)	130 (83%)	23 (15%)	3 (2%)	6	27
5	AB	213/215 (99%)	193 (91%)	17 (8%)	3 (1%)	9	34
6	AA	206/208 (99%)	175 (85%)	30 (15%)	1 (0%)	24	57
7	AV	80/82 (98%)	70 (88%)	10 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AY	124/126 (98%)	107 (86%)	16 (13%)	1 (1%)	16	47
9	Aa	105/107 (98%)	91 (87%)	14 (13%)	0	100	100
10	Ab	82/84 (98%)	74 (90%)	8 (10%)	0	100	100
11	Ae	57/59 (97%)	46 (81%)	10 (18%)	1 (2%)	6	28
12	AJ	173/182 (95%)	155 (90%)	17 (10%)	1 (1%)	21	52
13	AE	261/263 (99%)	229 (88%)	29 (11%)	3 (1%)	11	39
14	AC	224/226 (99%)	207 (92%)	16 (7%)	1 (0%)	30	61
15	AG	235/237 (99%)	218 (93%)	16 (7%)	1 (0%)	30	61
16	AH	188/190 (99%)	160 (85%)	23 (12%)	5 (3%)	4	20
17	AW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
18	AI	204/206 (99%)	173 (85%)	25 (12%)	6 (3%)	3	19
20	CR	149/153 (97%)	136 (91%)	13 (9%)	0	100	100
21	CW	122/124 (98%)	95 (78%)	27 (22%)	0	100	100
22	Ag	302/313 (96%)	270 (89%)	31 (10%)	1 (0%)	36	67
23	AU	102/104 (98%)	90 (88%)	10 (10%)	2 (2%)	6	25
24	AK	96/98 (98%)	71 (74%)	20 (21%)	5 (5%)	1	10
25	AM	122/124 (98%)	94 (77%)	26 (21%)	2 (2%)	7	30
26	AS	135/137 (98%)	119 (88%)	15 (11%)	1 (1%)	18	49
27	Ad	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
28	AR	124/126 (98%)	106 (86%)	16 (13%)	2 (2%)	7	30
29	AP	117/127 (92%)	101 (86%)	11 (9%)	5 (4%)	2	12
30	AT	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
31	AZ	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	9	34
32	Ac	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
33	AD	221/227 (97%)	198 (90%)	22 (10%)	1 (0%)	24	57
34	Af	69/71 (97%)	57 (83%)	10 (14%)	2 (3%)	3	19
35	AF	189/191 (99%)	164 (87%)	24 (13%)	1 (0%)	24	57
36	AQ	139/141 (99%)	122 (88%)	15 (11%)	2 (1%)	9	34
37	Cz	188/217 (87%)	169 (90%)	19 (10%)	0	100	100
38	CO	200/202 (99%)	191 (96%)	8 (4%)	1 (0%)	24	57
39	CL	208/210 (99%)	192 (92%)	14 (7%)	2 (1%)	12	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	CV	131/133 (98%)	121 (92%)	9 (7%)	1 (1%)	16	47
41	CM	137/139 (99%)	121 (88%)	16 (12%)	0	100	100
42	Ca	145/147 (99%)	126 (87%)	17 (12%)	2 (1%)	9	34
43	CN	201/203 (99%)	187 (93%)	14 (7%)	0	100	100
44	CI	197/213 (92%)	173 (88%)	23 (12%)	1 (0%)	24	57
45	CD	287/289 (99%)	263 (92%)	23 (8%)	1 (0%)	36	67
46	CQ	186/188 (99%)	163 (88%)	22 (12%)	1 (0%)	24	57
47	CA	253/255 (99%)	231 (91%)	22 (9%)	0	100	100
48	CS	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
49	CT	157/159 (99%)	141 (90%)	16 (10%)	0	100	100
50	CP	150/152 (99%)	142 (95%)	8 (5%)	0	100	100
51	CU	110/112 (98%)	91 (83%)	18 (16%)	1 (1%)	14	44
52	CX	119/121 (98%)	109 (92%)	7 (6%)	3 (2%)	4	21
53	CY	131/133 (98%)	122 (93%)	8 (6%)	1 (1%)	16	47
54	CZ	133/135 (98%)	117 (88%)	15 (11%)	1 (1%)	16	47
55	Cr	135/137 (98%)	107 (79%)	25 (18%)	3 (2%)	5	24
56	Ch	121/123 (98%)	105 (87%)	15 (12%)	1 (1%)	16	47
57	Cb	65/78 (83%)	59 (91%)	4 (6%)	2 (3%)	3	18
58	CB	390/397 (98%)	351 (90%)	35 (9%)	4 (1%)	12	41
59	CF	227/229 (99%)	215 (95%)	9 (4%)	3 (1%)	9	35
60	Cc	98/100 (98%)	92 (94%)	5 (5%)	1 (1%)	12	41
61	Cd	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
62	Ce	131/133 (98%)	122 (93%)	8 (6%)	1 (1%)	16	47
63	Cf	107/109 (98%)	90 (84%)	15 (14%)	2 (2%)	6	27
64	Cg	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
65	Ci	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	41
66	Cj	88/90 (98%)	78 (89%)	9 (10%)	1 (1%)	11	39
67	Ck	67/69 (97%)	58 (87%)	9 (13%)	0	100	100
68	Cl	48/50 (96%)	48 (100%)	0	0	100	100
69	CC	356/368 (97%)	301 (85%)	51 (14%)	4 (1%)	11	39
70	Cm	50/52 (96%)	46 (92%)	3 (6%)	1 (2%)	6	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	Cn	23/25 (92%)	23 (100%)	0	0	100	100
72	Cp	88/90 (98%)	82 (93%)	6 (7%)	0	100	100
73	Co	103/105 (98%)	87 (84%)	15 (15%)	1 (1%)	12	41
74	CJ	166/168 (99%)	154 (93%)	10 (6%)	2 (1%)	10	37
75	CH	189/191 (99%)	177 (94%)	11 (6%)	1 (0%)	24	57
76	CE	260/262 (99%)	200 (77%)	53 (20%)	7 (3%)	4	20
77	CG	244/246 (99%)	218 (89%)	23 (9%)	3 (1%)	10	37
All	All	11455/11704 (98%)	10164 (89%)	1184 (10%)	107 (1%)	16	44

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AO	56	VAL
4	AL	23	VAL
13	AE	164	LEU
16	AH	66	VAL
18	AI	120	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AO	106/106 (100%)	100 (94%)	6 (6%)	18	49
2	AX	114/114 (100%)	109 (96%)	5 (4%)	25	56
3	AN	130/130 (100%)	123 (95%)	7 (5%)	20	50
4	AL	142/142 (100%)	135 (95%)	7 (5%)	22	53
5	AB	196/196 (100%)	188 (96%)	8 (4%)	27	59
6	AA	174/174 (100%)	160 (92%)	14 (8%)	11	37
7	AV	66/66 (100%)	64 (97%)	2 (3%)	36	65
8	AY	108/108 (100%)	100 (93%)	8 (7%)	13	40
9	Aa	90/90 (100%)	85 (94%)	5 (6%)	19	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Ab	76/76 (100%)	72 (95%)	4 (5%)	20	51
11	Ae	48/48 (100%)	47 (98%)	1 (2%)	47	71
12	AJ	156/157 (99%)	149 (96%)	7 (4%)	24	56
13	AE	225/225 (100%)	215 (96%)	10 (4%)	25	56
14	AC	190/190 (100%)	183 (96%)	7 (4%)	30	61
15	AG	207/207 (100%)	201 (97%)	6 (3%)	37	66
16	AH	170/170 (100%)	156 (92%)	14 (8%)	10	36
17	AW	112/112 (100%)	103 (92%)	9 (8%)	11	37
18	AI	178/178 (100%)	172 (97%)	6 (3%)	32	63
20	CR	134/134 (100%)	129 (96%)	5 (4%)	30	61
21	CW	103/103 (100%)	98 (95%)	5 (5%)	22	53
22	Ag	265/272 (97%)	257 (97%)	8 (3%)	36	65
23	AU	94/94 (100%)	92 (98%)	2 (2%)	47	71
24	AK	89/89 (100%)	83 (93%)	6 (7%)	15	43
25	AM	104/104 (100%)	96 (92%)	8 (8%)	12	38
26	AS	119/119 (100%)	111 (93%)	8 (7%)	15	43
27	Ad	47/47 (100%)	47 (100%)	0	100	100
28	AR	114/114 (100%)	112 (98%)	2 (2%)	51	73
29	AP	108/116 (93%)	106 (98%)	2 (2%)	50	73
30	AT	112/112 (100%)	108 (96%)	4 (4%)	31	62
31	AZ	66/66 (100%)	63 (96%)	3 (4%)	24	56
32	Ac	57/57 (100%)	54 (95%)	3 (5%)	20	51
33	AD	187/190 (98%)	184 (98%)	3 (2%)	55	75
34	Af	64/64 (100%)	62 (97%)	2 (3%)	35	64
35	AF	161/161 (100%)	155 (96%)	6 (4%)	30	61
36	AQ	117/117 (100%)	109 (93%)	8 (7%)	14	42
37	Cz	170/196 (87%)	165 (97%)	5 (3%)	37	66
38	CO	173/173 (100%)	166 (96%)	7 (4%)	28	60
39	CL	176/176 (100%)	172 (98%)	4 (2%)	44	70
40	CV	102/102 (100%)	99 (97%)	3 (3%)	37	66
41	CM	118/118 (100%)	110 (93%)	8 (7%)	14	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	Ca	120/120 (100%)	111 (92%)	9 (8%)	12	39
43	CN	171/171 (100%)	167 (98%)	4 (2%)	44	70
44	CI	171/180 (95%)	160 (94%)	11 (6%)	16	44
45	CD	243/243 (100%)	236 (97%)	7 (3%)	37	66
46	CQ	165/165 (100%)	154 (93%)	11 (7%)	15	43
47	CA	197/197 (100%)	188 (95%)	9 (5%)	24	55
48	CS	156/156 (100%)	152 (97%)	4 (3%)	40	68
49	CT	139/139 (100%)	133 (96%)	6 (4%)	26	57
50	CP	133/133 (100%)	128 (96%)	5 (4%)	29	60
51	CU	102/102 (100%)	98 (96%)	4 (4%)	28	60
52	CX	109/109 (100%)	103 (94%)	6 (6%)	19	50
53	CY	123/123 (100%)	118 (96%)	5 (4%)	27	59
54	CZ	117/117 (100%)	113 (97%)	4 (3%)	32	63
55	Cr	121/121 (100%)	108 (89%)	13 (11%)	6	25
56	Ch	110/110 (100%)	105 (96%)	5 (4%)	24	56
57	Cb	58/66 (88%)	55 (95%)	3 (5%)	21	51
58	CB	341/345 (99%)	331 (97%)	10 (3%)	37	66
59	CF	198/198 (100%)	193 (98%)	5 (2%)	42	69
60	Cc	85/85 (100%)	80 (94%)	5 (6%)	18	48
61	Cd	102/102 (100%)	91 (89%)	11 (11%)	6	25
62	Ce	119/119 (100%)	108 (91%)	11 (9%)	8	31
63	Cf	88/88 (100%)	84 (96%)	4 (4%)	24	56
64	Cg	98/98 (100%)	91 (93%)	7 (7%)	13	41
65	Ci	87/87 (100%)	83 (95%)	4 (5%)	24	55
66	Cj	75/75 (100%)	73 (97%)	2 (3%)	39	67
67	Ck	64/64 (100%)	60 (94%)	4 (6%)	16	45
68	Cl	47/47 (100%)	44 (94%)	3 (6%)	16	44
69	CC	298/305 (98%)	283 (95%)	15 (5%)	22	53
70	Cm	48/48 (100%)	47 (98%)	1 (2%)	47	71
71	Cn	24/24 (100%)	23 (96%)	1 (4%)	26	58
72	Cp	74/74 (100%)	69 (93%)	5 (7%)	14	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Co	93/93 (100%)	85 (91%)	8 (9%)	10	34
74	CJ	142/142 (100%)	135 (95%)	7 (5%)	22	53
75	CH	170/170 (100%)	165 (97%)	5 (3%)	37	66
76	CE	232/232 (100%)	211 (91%)	21 (9%)	9	32
77	CG	209/209 (100%)	202 (97%)	7 (3%)	33	63
All	All	9997/10070 (99%)	9527 (95%)	470 (5%)	25	55

5 of 470 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	Ca	77	LYS
76	CE	69	TYR
49	CT	61	THR
75	CH	21	LYS
68	Cl	17	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 130 such sidechains are listed below:

Mol	Chain	Res	Type
73	Co	105	GLN
75	CH	98	HIS
36	AQ	97	GLN
36	AQ	35	ASN
75	CH	156	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	B2	1748/1861 (93%)	524 (29%)	37 (2%)
78	A5	1662/3889 (42%)	500 (30%)	58 (3%)
78	A6	1993/3889 (51%)	578 (29%)	45 (2%)
79	A7	120/121 (99%)	21 (17%)	0
80	A8	156/157 (99%)	39 (25%)	3 (1%)
81	BC	74/75 (98%)	26 (35%)	2 (2%)
All	All	5753/9992 (57%)	1688 (29%)	145 (2%)

5 of 1688 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
19	B2	2	A
19	B2	3	C
19	B2	4	C
19	B2	20	G
19	B2	21	U

5 of 145 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
78	A6	3876	A
78	A6	4997	G
78	A6	4072	C
78	A6	4699	U
78	A5	505	G

#### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

#### 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	A5	11
78	A6	6
19	B2	2
20	CR	1



The worst 5 of 20 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CR	83:GLY	C	120:TYR	N	39.03
1	A5	1440:U	O3'	1447:C	P	24.44
1	A6	4034:G	O3'	4039:G	P	20.91
1	A6	3292:G	O3'	3572:G	P	20.30
1	A5	1703:C	O3'	1720:C	P	18.79

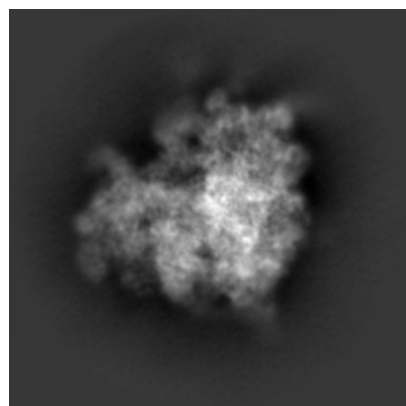
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74615. These allow visual inspection of the internal detail of the map and identification of artifacts.

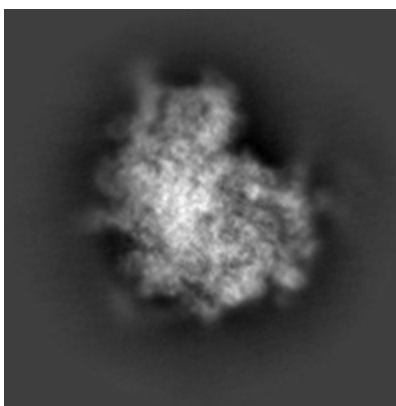
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

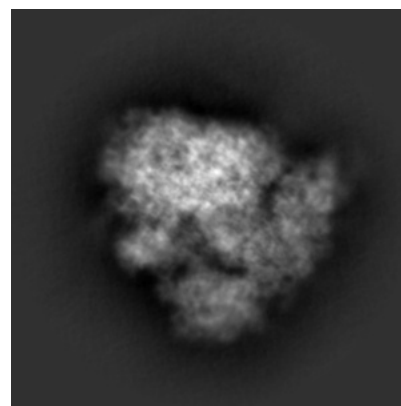
#### 6.1.1 Primary map



X

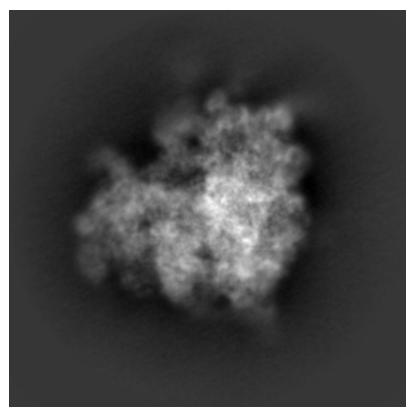


Y

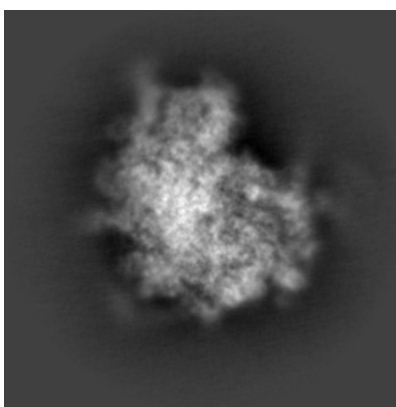


Z

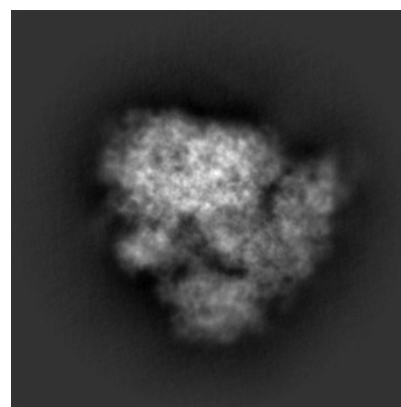
#### 6.1.2 Raw map



X



Y

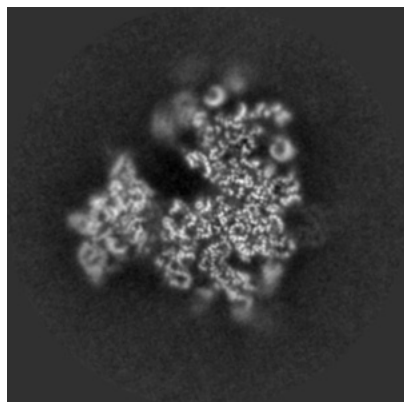


Z

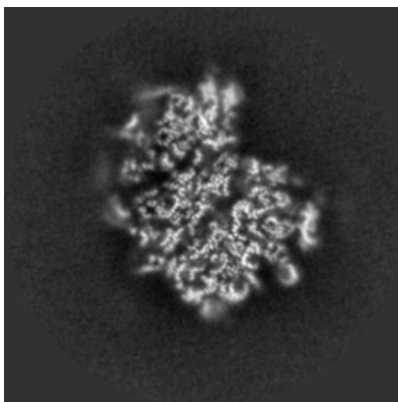
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

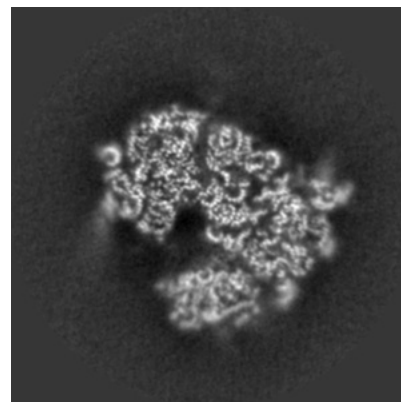
### 6.2.1 Primary map



X Index: 210

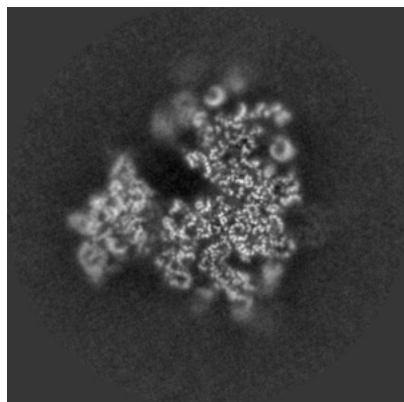


Y Index: 210

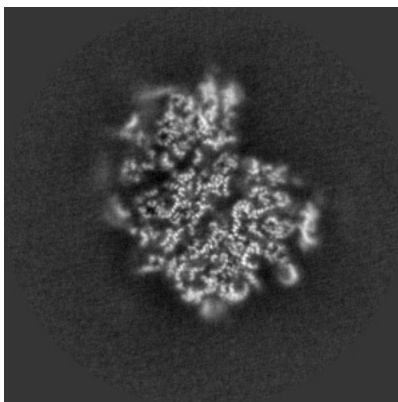


Z Index: 210

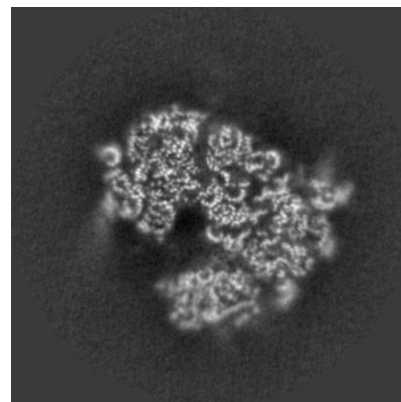
### 6.2.2 Raw map



X Index: 210



Y Index: 210

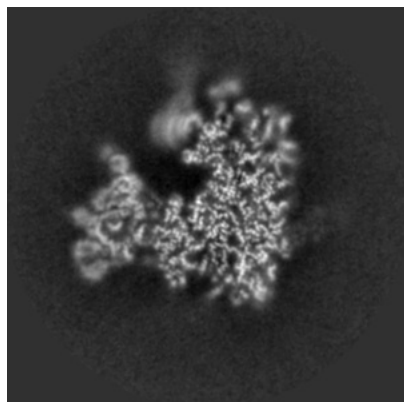


Z Index: 210

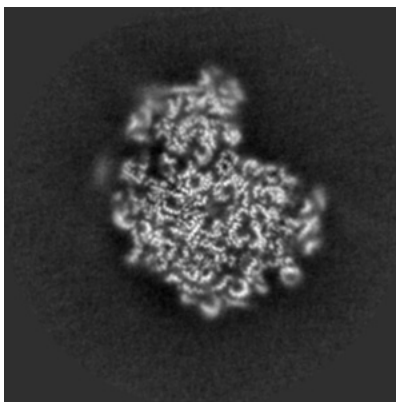
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

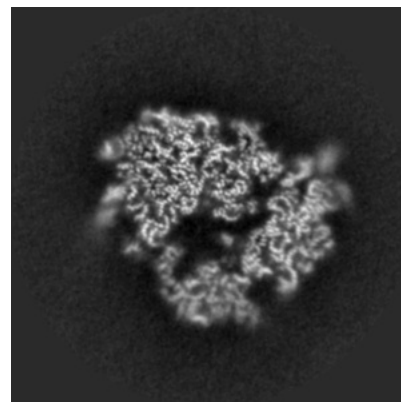
### 6.3.1 Primary map



X Index: 221

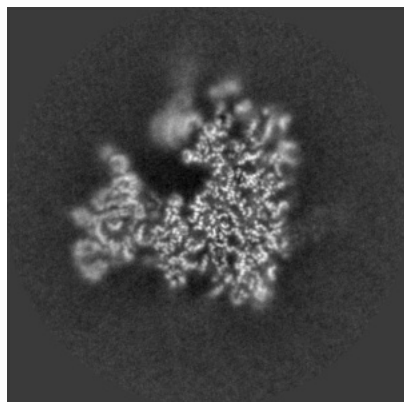


Y Index: 217

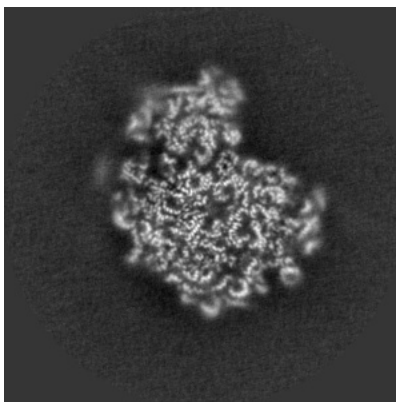


Z Index: 221

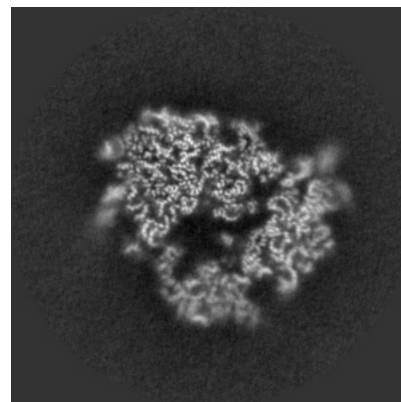
### 6.3.2 Raw map



X Index: 222



Y Index: 217

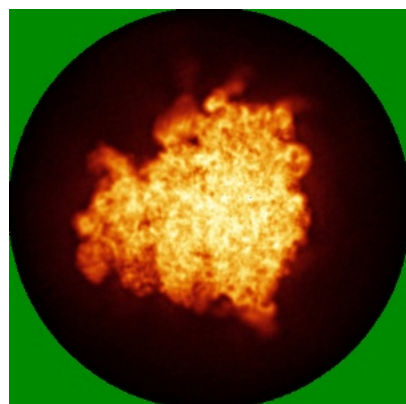


Z Index: 221

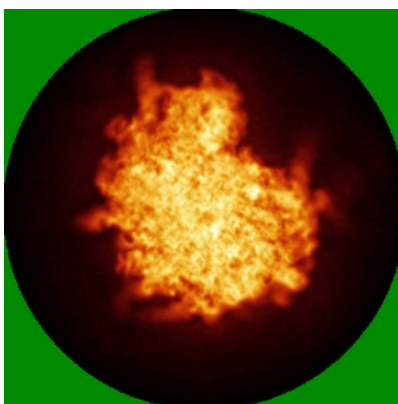
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

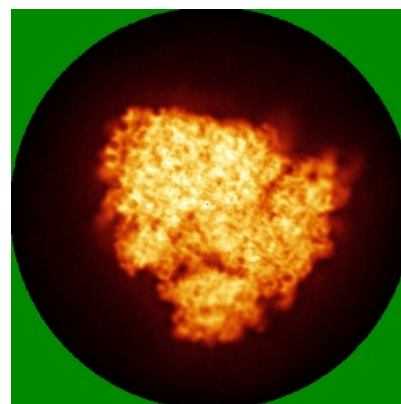
### 6.4.1 Primary map



X

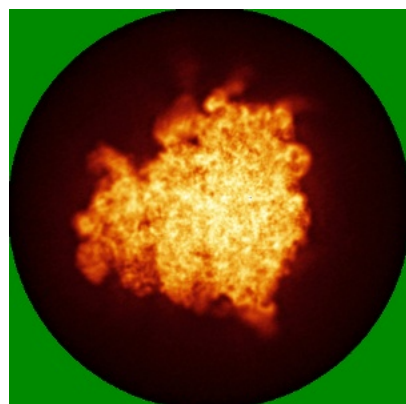


Y

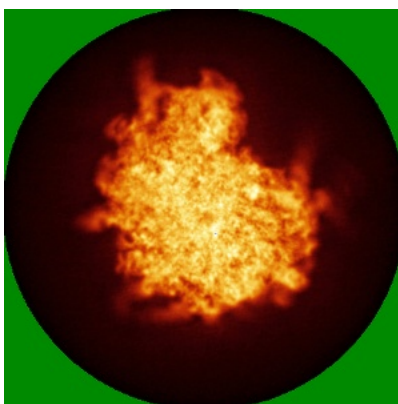


Z

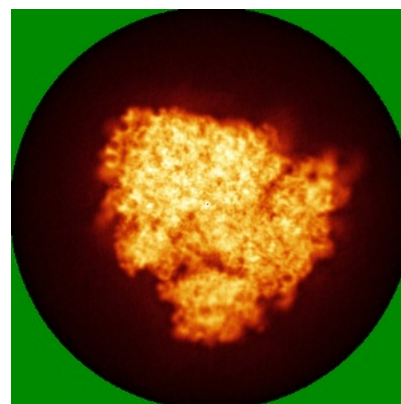
### 6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

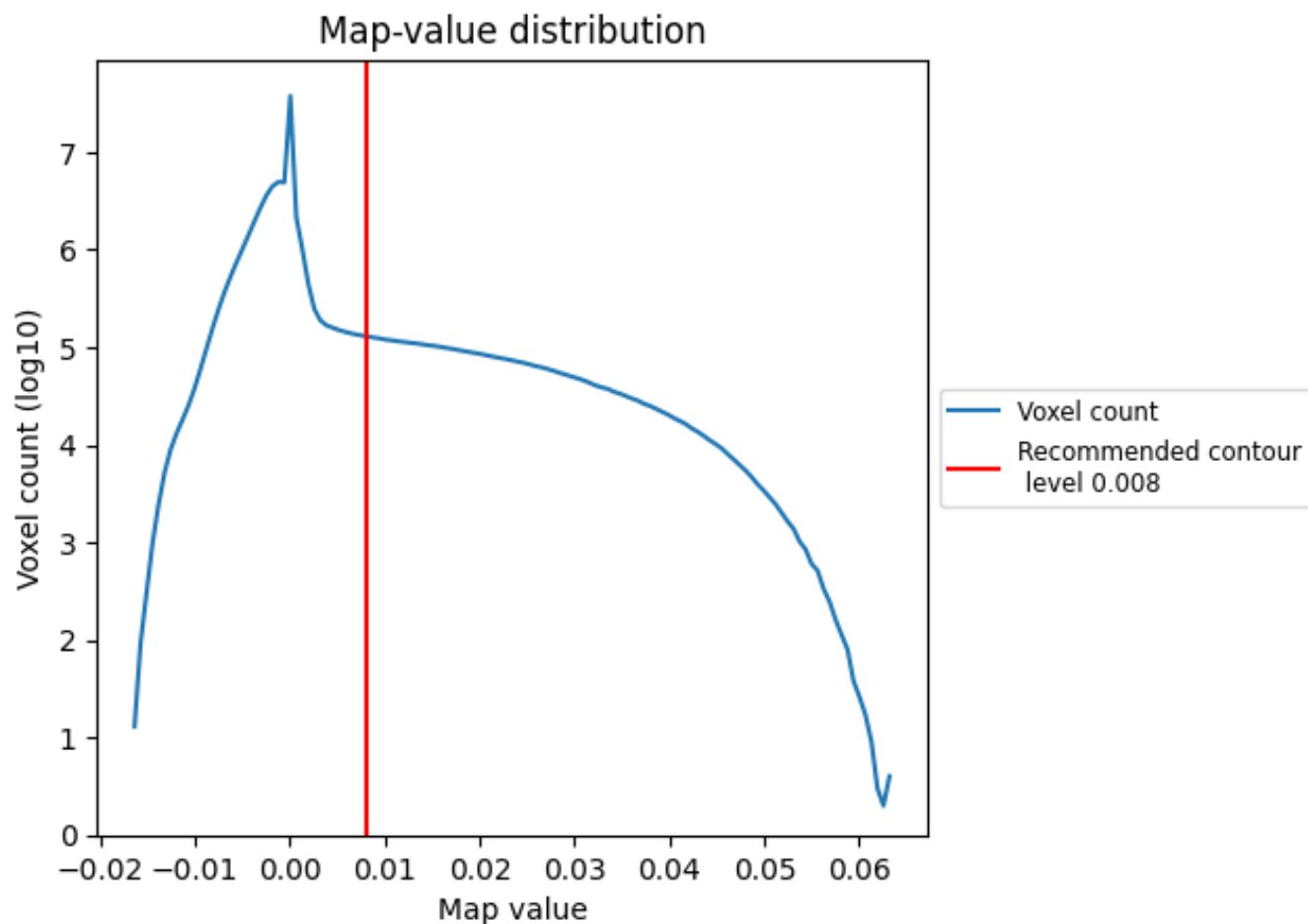
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

This section contains the results of statistical analysis of the map.

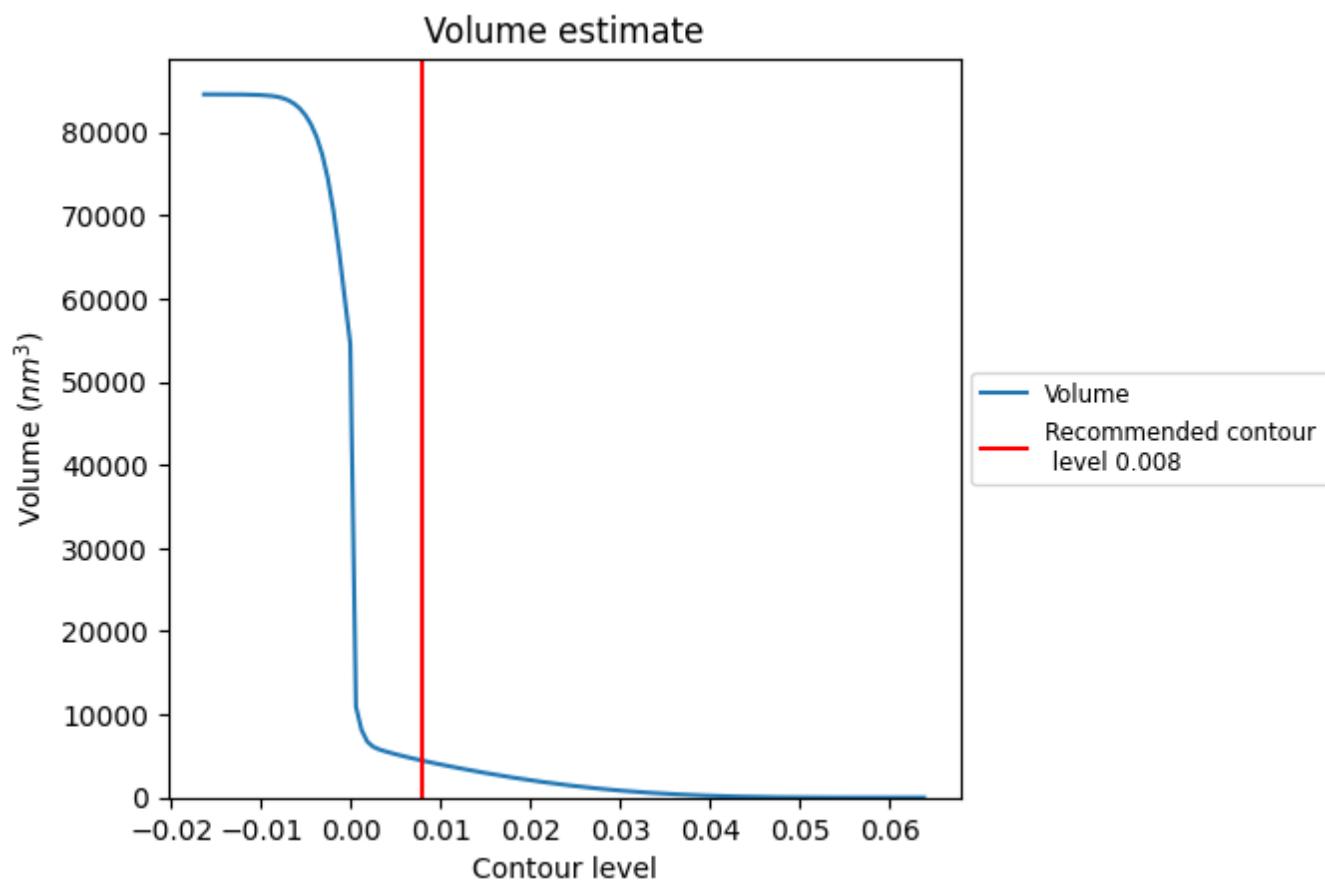
### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



## 7.2 Volume estimate [i](#)

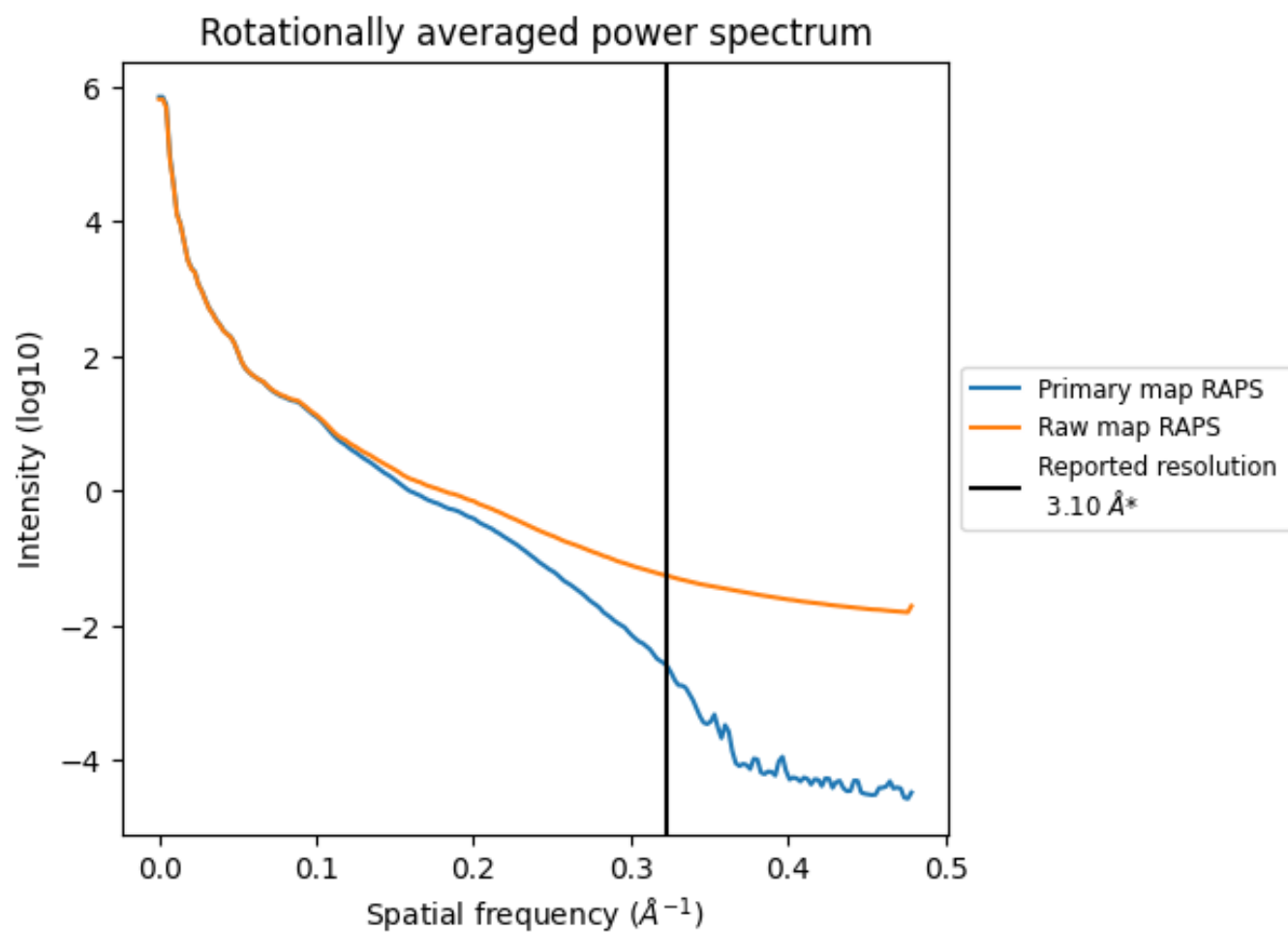


The volume at the recommended contour level is 4431 nm<sup>3</sup>; this corresponds to an approximate mass of 4002 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



### 7.3 Rotationally averaged power spectrum ⓘ

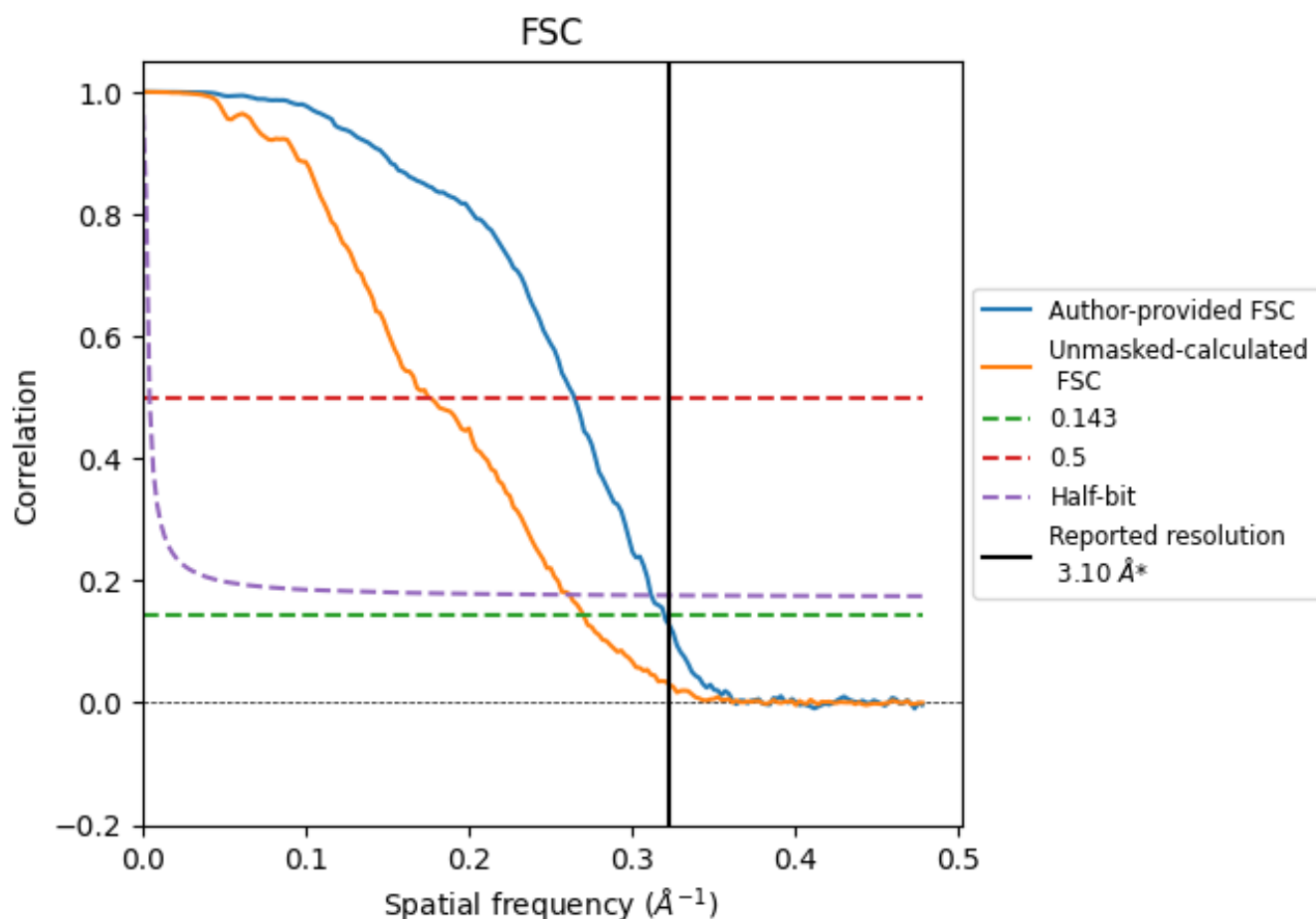


\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.323 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

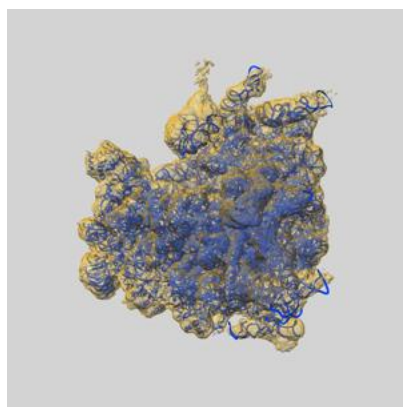
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.77	3.20
Unmasked-calculated*	3.69	5.70	3.81

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.69 differs from the reported value 3.1 by more than 10 %

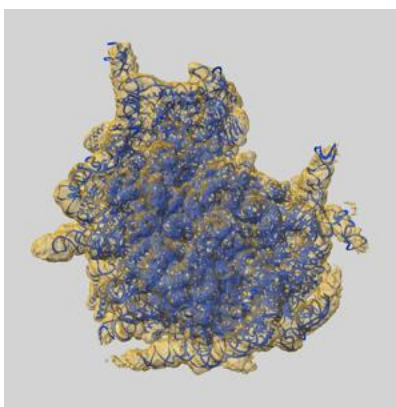
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74615 and PDB model 9ZRG. Per-residue inclusion information can be found in section 3 on page 19.

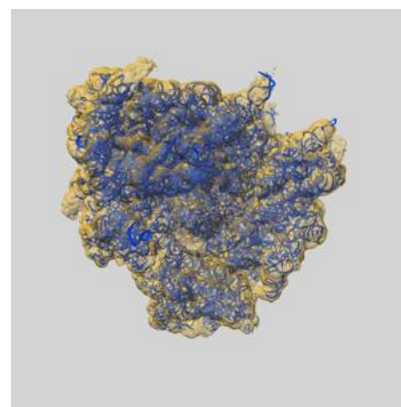
### 9.1 Map-model overlay [i](#)



X



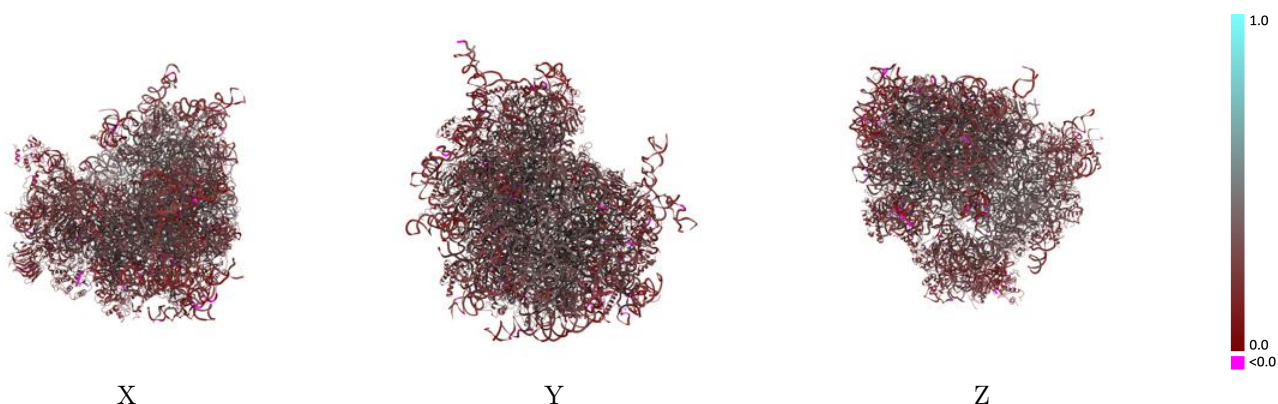
Y



Z

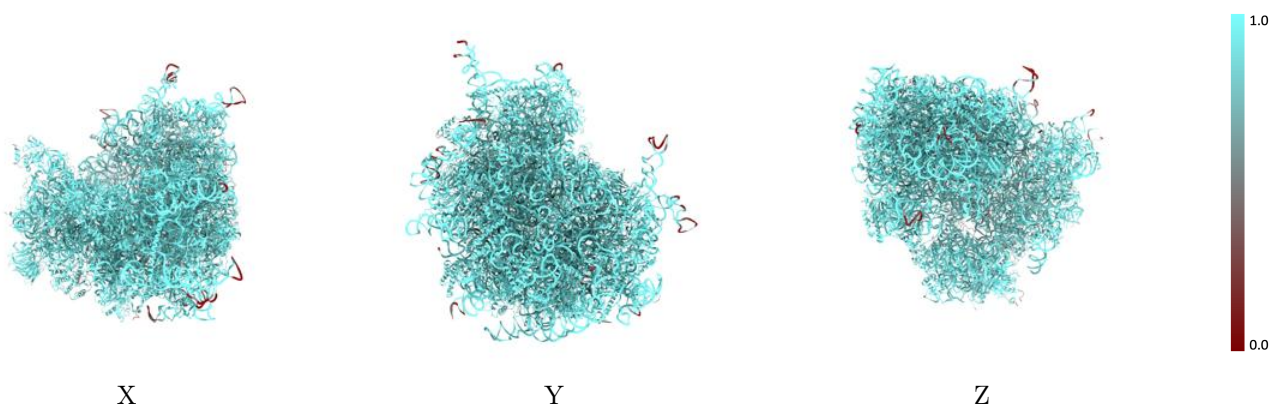
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



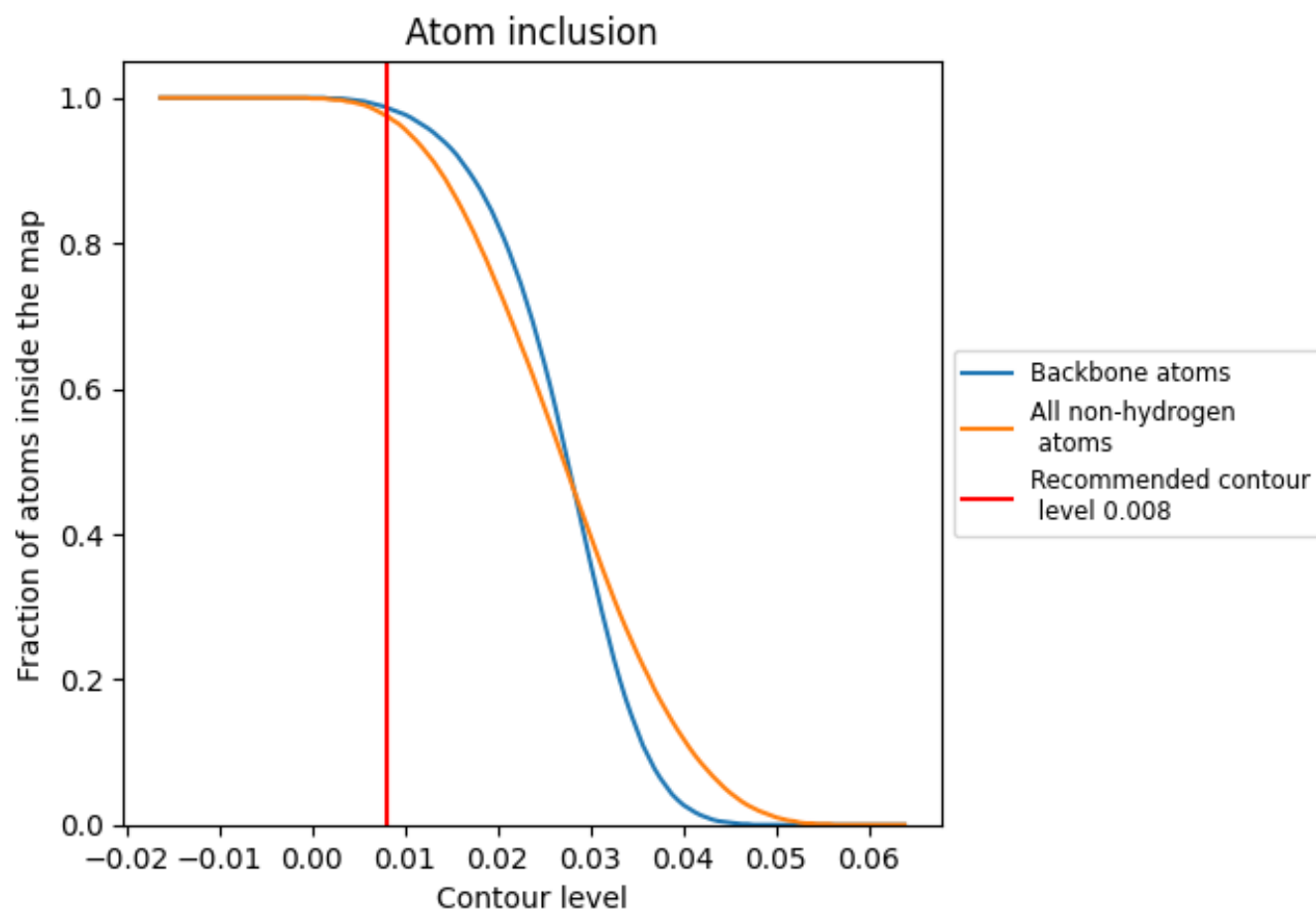
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.008).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9750	0.2990
A5	0.9860	0.3110
A6	0.9870	0.3360
A7	0.9960	0.3370
A8	0.9930	0.3320
AA	0.9680	0.2540
AB	0.9520	0.2780
AC	0.9460	0.3020
AD	0.9600	0.2340
AE	0.9810	0.2850
AF	0.9720	0.2190
AG	0.9810	0.2330
AH	0.9500	0.2420
AI	0.9610	0.2760
AJ	0.9700	0.2720
AK	0.9540	0.2040
AL	0.8920	0.3070
AM	0.9030	0.1550
AN	0.9370	0.2890
AO	0.9590	0.2870
AP	0.9750	0.1960
AQ	0.9940	0.2060
AR	0.9550	0.2020
AS	0.9840	0.2040
AT	0.9890	0.2030
AU	0.9610	0.2110
AV	0.9540	0.2570
AW	0.9620	0.3190
AX	0.9660	0.3420
AY	0.9810	0.2400
AZ	0.9780	0.1950
Aa	0.9050	0.2870
Ab	0.9400	0.2780
Ac	0.9200	0.2430
Ad	0.9810	0.2210



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Chain	Atom inclusion	Q-score
Ae	 0.9120	 0.2650
Af	 0.9720	 0.1490
Ag	 0.9840	 0.1960
B2	 0.9920	 0.3010
BC	 0.9810	 0.2310
CA	 0.9260	 0.3620
CB	 0.9720	 0.3290
CC	 0.9600	 0.3290
CD	 0.9860	 0.2600
CE	 0.9700	 0.2250
CF	 0.9490	 0.3180
CG	 0.9560	 0.2650
CH	 0.9660	 0.2960
CI	 0.9590	 0.3370
CJ	 0.9740	 0.2570
CL	 0.9680	 0.3060
CM	 0.9810	 0.2770
CN	 0.9700	 0.3360
CO	 0.9260	 0.3100
CP	 0.9670	 0.3470
CQ	 0.9390	 0.3300
CR	 0.8760	 0.1640
CS	 0.9760	 0.3100
CT	 0.9560	 0.3330
CU	 0.9250	 0.2310
CV	 0.9460	 0.3570
CW	 0.9160	 0.1890
CX	 0.9780	 0.3130
CY	 0.9790	 0.3020
CZ	 0.9790	 0.2840
Ca	 0.9740	 0.3540
Cb	 0.9570	 0.2970
Cc	 0.9310	 0.2850
Cd	 0.9690	 0.3020
Ce	 0.9320	 0.3510
Cf	 0.9480	 0.3350
Cg	 0.9690	 0.3090
Ch	 0.9740	 0.2770
Ci	 0.9540	 0.2620
Cj	 0.9400	 0.3420
Ck	 0.9480	 0.2680
Cl	 0.9650	 0.3260

*Continued on next page...*



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Chain	Atom inclusion	Q-score
Cm	 0.9760	 0.3230
Cn	 0.8900	 0.3100
Co	 0.9210	 0.3240
Cp	 0.9060	 0.3460
Cr	 0.9050	 0.2720
Cz	 0.9400	 0.0930